

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCACCAC**ATG**TTGGCTGCAAGGCTGGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTCACCAAGGCCTCCCCTGTTGTGAAGAATTCCATCACGAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAAATTTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAACTCAAAGAGGCAGCATTTGGAACCATCGATGGAAAAAATATTTAAAAAT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCAATTTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCAATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCTGTCTCATGAACCTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCGAGGCCCAAAGCATCTTCTGTTGGTGTACATTTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCCAAGTAAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACCTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAA**TG**
AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTTTAAATGGGGCAGATATGC
 ATTAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCAT
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGCTCGCCTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAAATAAGCACACACATTTCAATTCATGTTTGGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAACATAAGTTTGTGTCATGAGAATGTAAGTCTTTTTCTACTTTAAAA
 TTTAGTAGGTTTCACTGAGTAACATAAATTTAGCAAACCTGTGTTTGCATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACCAAGTGGTCATTGTTACATTCATT
 GCTGAACCTTAACAAAACGTGTTTCATCTGAAACAGGCACAGGTGATGCATTTCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAAATATAGATGTGGTCATGTTTGAAGTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTTAAACATATCTCAAGAGAAAATATCAAGCATGAATATGTTGCTTTTCCAG
 AATACAAACAGTATACTCATG

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGCTCTCCGCCTTCTGCAT
 CGCGGGCTTCGGCGGGCTTCACCTAGACACCTAACAGTCCGGAGCGCGGCCGCTCGTGAGGG
 GGTCCGCGACGGGAGTCCGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCCGAAGATGTCGG
 ACATCCGAGACTGGTTTCAGGAGCATCCCGGCGATCACGGCTATTGGTTCCGCGCCACCGCTG
 CCGGTGCCCTTGGTCCGCCAACTCCGGCTCATCAGCCCGGCTACCTCTTCCCTCTGGCCCGA
 AGCCTTCCCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTCTTCTTCCCTTGTGG
 CTCCAGGACATGGATTTCTTTATTTGGTCAATTTATATTTCTTATTCAGTATTCACGCGA
 CTTGAAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGTATCA
 TGTGAGTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTTGATCATTTTGGTTTGGGA
 ACACGATTTAAGGCCCTGCTATTTACCTGGGTATCCTTGGATTCAACTATATCATCCGAGG
 CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTCCTAATGTTCA
 GATACCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCCATGAGGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGCGAGCG
 TGCTGATCAGAATGGCGGAGGCGGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC
 AGTGAAGGGGCGGCCTCGGGCAGCCGCTCTCTCAAGCCACATTTCTCCAGTGCTGGGTG
 CACTTAACAACCTGCGTTCTGGCTAACACTGTGGACCTACCCACACTGAATGTAGTCTTTC
 AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATAAGTGTTCCACAGTTTTCACGAT
 TCTCATCTCAAGTCCCTTACTGCTGTGAAGAACAAATACCAACTGTCGAATTTGCAAACTGAC
 TACATTTTGTGTCTCTCTCTCTCCCTTTCCGCTCTGAATATGGGTTTGTAGCGGTCTCT
 AATCTGCTGGCATGCTGAGCTGGGGCTGGGTCACCAACCCCTCCCAAAAGGACCTTATGCTCTT
 TCTTGCACACATGCCCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG
 CCAATAAAATTTGCTCGCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGTC
 ACAACATCATATTACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
 AAGACAGCCACGGATGACGCGTTTCTCAGCTTTTGGAAATGCTTGCAGCTGACATCGGTGTT
 AACCGTTTGCCACTCTTCAGATATTTTTTATAAAAAAGTACCACCTGAGTTGATGAGGGCCA
 CAGATTTGTTTATTAATGAGTACGAGGGTTGGTGTGGGTGTTTGTTCCTGAGCTAAGTGGA
 TCAAGACTGTAGTGGAGTTGCACCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCCT
 TTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCAATG
 ATTTCCCATTTCAATCTCATTTCTGGATATGTGTTCAATTGAGTAAAGAGGAGAGACCCCTATA
 CGCTATTTAAATGTCACTTTTTCGCTATCCCCGCTTTTGTGTCATGTTTCAATTAATGT
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTGAGGGTGTTGA
 TTTTGTAGTCAATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTT
 TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCA
 TGGCTTTTACACAGTTATTTTTTTTATGACGTTATCTGAAAGCAGACTGTTTAGGAGCAGT
 ATTGAGTGGCTGTGCACACTTTTGGGCAACTAAAAAGGCTTCAAAACGTTTGTATCAGTTTCTT
 TTCAGGAACATTTGCTCTAACAGTATGACTATCTTTCCGCACTTCTAAACAGCTGTGAT
 GTGTGTTATCTTACGAAATGAGAGTTGGCAACAACTTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGAGAGCTGGAACCTTAACTGATCA
 TGTTTTGTGTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAATTTTAGAGGCCATTACT
 CCAATTTATGTGCAGTACACTCATTTGTACAGGCGTGGAGACTCATTTGATGTATGATAAGAATA
 TTTCTGACAGTGAGTGACCGGAGTCTCTGGTGTACCCCTTTACCAGTCAGCTGCCTGCGAG
 CAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAATTTTCAGTTCCAGGCGCAAAATGTT
 ATGAAGTTATTTCTCTTAAACATGGTTAGGAAGCTGATCAGCTTATTTGATTTGTTCTCTGGAT
 ATGTTTCTGGAATAATTTTACCAAAACAGCTATTTGAGTTTTGACTTTGACAAAGGCAAAACA
 TGACAGTGGATTCCTTTTACAAATGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC
 TTTTGTGAACTAATCCTTTTATTTGTTAAAAATGTAAATTAATGTCGCACTTG

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FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGLGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCCGCGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACGTGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGCCCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCTTGCC
 CCTTTGGGGCGGGATGGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGAAGTCTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGCGATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCCTTGTTTTTGTATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
 GAGGGAAGTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCAGGTGAAGCTGCAATAATG
 AATAATTTCCAAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCTCCTCC
 CACAAAAGGCCTGAAGATTCTTGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAAG
 GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAAGTTATTAATAAGTA
 ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAADFTIFKAMMVQKNIEMQLQAIRIIQERNGLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKQLSEAKTEEPTVHSSEAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAGCATGCACTTCTCCTCTTGAAAAGACCATACATCAGAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAACATTTGAAATGCAGCTGCAAGCCATTCCAATAATTCAAAGAGAGAATGGTGATTTA
CTGACTGCTTAAACCAGTCGGCTGTGTTGTGGTCACTTGAGTGAACCGAAGATGAAAAT
CCTGAGGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCGAGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTTCGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGGTTCTTCCACTAGAAGCTCTCTGAGGGAGGTAATAAAAAAG
 AGTGGAAATGGAAAAACAGTGTCTAGTCATCTGTAATATGCTCTTGTCTCAACAATGTATAC
 ATTCTGCTAGGTGCCATATTCATGCTTTAAGCTCAAGTCGATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAACAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAG
 AAAATTTGAAATATGCTTCCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCCTGCCT
 TTTCTTATTTCTGGATACTTGATTGTCTTCTATGCTCTGCTATCTTCAACAGGCATG
 GCTGTTATCTCTCAAATTTAGCATTATAACAACAGCTCTTCTATTCTCAGGATAGTGTGAA
 GAGGCGCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAACTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCC
 TTTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAAGACAATTG
 TACAGCAAGAAGATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAAGATACTGAAGGAGGGGAACAGCTCAGTGAAGAGATCTTCATACA
 GAACAGCAAACTCTATTTCTTTGGCATCTGTTTAAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGTGATCAGATTAAGAAGTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTTGTAAGTGCATTCAGGGCCCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTTATGGGCCAGGTACCAGTGTCTATATACAACAGTGTCTGTCCTGG
 TCTTTGACTTCAGGCCCTCCTGGAATTTTTCTTGAAGCCCCATCAGTCTCTTCTCTATA
 TTTATTTATAATGCCAGCAAGCCCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAACTCTTGGGAGCGTCCAGTGGGGATGGAGAAGAACTAGAAAAGACTTA
 CCAAAACCAAGAGTGATGAGTCAGATGAAGATACTTCTTAAGTGGTACCCACATAGTTTGCA
 GCTCTCTTGAACCTTATTTTTCACATTTTCAGTGTGTTGTAATATTTTACTTTTTCAGTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGTCATATATCTAGCTACTCCCTAAATGGTT
 CCAATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCCTTCAAGCTTCCAAAAAAGTGTGAATAATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
 TCTCCCTTTTAAACCTATAAAAAGCTAGGTTGTCTCTGAAATTTGAGGCCCTAGAGATAGT
 CATTTTGAAGTAAGAGCAGCAAGGGACCCCTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGTTGGGATGATGTAGTCTGTGCTAAATTTTGTGCTGAAGAAGCAGT
 TTCTCAGACACAAATCTCAGAATTTTAAATTTTGAAGAAATTCATGGGAAATTTGGATTTTTGT
 AATAATCTTTGATGTTTTAAACATTGGTTCCTAGTCCACCATAGTTACCAGTGTATTTTA
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
 GTCATTACTCTGAATTTATTACATTTTGGAGAATAAGAGGGCATTTTTTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTCCAAAGATTGAAATGCTGGCTCAGATCATAC
 CAGATTGTGTCAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAAAACATATGTGACTTTTAACTGATGATGAATATTAATCACTCTAAAAATGAAAGACC
 AGTAATATATAAGTCACTTTTACAGTGCTACTTCACACTTAAAGTGCATGGTATTTTCTATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAGCAAAACAAAAGTGACTTGCTCAGGGCTATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGCGAGCCCTGTATGTTTACAGACTACCATGTGAATATGAGCTTTATGGTGT
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAAATATACTATTATATAATTCATTGTGATATCCACAATAATATGACTGGCAAGAAATTG
 GTGGAAATTTGTAATTAATAATATTATAAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
 IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFVSALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

CGTGCGCTGCGCAATGGGTGTGCGGTCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCATAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAACAGTGAATGGAA
AAACAGTGTGTAGTCATCCTGTAATATGTCCTTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTCA TTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTC TGCCAATGAAG
AAAACAAGTATGATTATCTTCCAAC TACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCTCGGAAGGAATTCTCTGATTTCA TGAAGTGGTCCATTCTCGCCTTTCTTTATTTC
TGGATAACTTGATTGCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAAATTTTAGCATTATAACAACAGCTCTTCTATT CAGGATAGTGTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAACCTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTTGGGGGCGAGGAGCAT
 CCCGCTCTACGAGTCCCAAGCGGCGTGGCCCGCGGGTTCATGGCCAAAGGAGAAGGCGCGGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTGCAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACGAGTGACGGGCTGTGCCCTGGGTTTCTTCTTCAGATCTAC
 CTATTG**CATG**CTGGCTCAGGTGGGCCCTTCTCTGCCCTCCATCATCCTGTTTGTGGGCCGAGC
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCACGCCCCCTGGCCGTCATTGCCCTACTTCCTC
 ATCTGGTTCTGCGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCCT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATTGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAATCGTGGGCCAAGCAGACACGCCCTTGTTTCCAGG
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATACACATGGCACCACCTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCTCCTGATCCTGGGCGTGGCGGAGCAGAGAAACCCATGAAGCCACGACGCTG
 AGCCAATCGCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTT
 ATTACTGGCTTCTCTTCACTCCTTGGCTTTCATGCTGGAGGGAACTTTGCTTGTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAACCATTTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCGCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTACCAGGTTTGCCCTCTGGAGTGTC
 ACTGGGCATTTTACCCCTCAGTCTGGACTTTGCAAGGTACCAGACCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCTGCTGCTCTTCAAATGTACCCCATGTATGAGGAGAGGCGGCGGCAGATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCT**TAG**GGCCCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGTCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCCAAGACACTGTCTGCTCACTGTGGGGCCGGCTGCTCTG
 TGGCTCTGCTCTCCCTCTGCTTGCCTGTGGGGCCAAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGGCTAGCCCGGAACATAATGTAGAACCCTTTTTTTTACAGGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATATGCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

MWLRWALS L P S S C L W A E P G M P S Q T P W W A S A S A N P P G P A W A L C P G S S S P R F W P S L P T S S S G
S C P T S H T A R P I G T C F S I A S L K Q W S R V S M F P T R L S P C S S A T E Q T E R D S A T A Y R M T E V L G T V L
G T A I Q Q G V I V G Q A D T P C F Q D F N S T V S A S Q S A N H T H G T T S H R E T Q K A Y L L A A G V I V C I Y I T C A V
I L I L G V R E Q R E P Y E A Q Q S E P I A Y F R G L R L V M S H G P Y I K L I T G F L F T S L A F M L V E G N F V L F C T
Y T L G F R N E F Q N L L A I M L S A T L T I P I Q W F L T R F G K K T A V Y V G I S S A V P F F I L V A L M E S N L I
I T Y A V A V A A G I S V A A F L P W S M L P D V I D D F H L K Q P H F H G T E P I F F S F Y V F T K F A S G V S L G
I T S L S L D F A G Y Q T R G C S P E R V K F T L N M L V T M A P I V L I L G L L L F K M Y P I D E R R R Q N K K A L
Q A L R D E A S S S G C S E T S D T E L A S I L

GGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGC GGAGCAGAGAACCCATGAAGCCAGCAGTCTGA
GCCAATCGCCTACTTCGGGGGCTACGGCTGGTCATGAGCCAGGCCATACATCAAACTTA
TTACTGGCTTCTCTTCACTTCCTTGGCTTTCATGCTGGTGAGGGGAACTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATATTACATATCGGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCTTGGTCCATGCTGCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAAACAGAAAACCTGTTAGAAATG
 GGTGGTTTCAGCAAGGCCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGCTACTTGGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTTCAGAAAAACAACCTTTTTTGTGTCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCTACCAAATG
 CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCAATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTTCATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA
 TTCCTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTGATAGATTATCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACCTTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTGTGTAAGCAGT
TACCAAGAATCTTCAACCCCTTCCCACAAAAGCTAATTGAGTACACGTTCTCTGTTGAGTACA
CGTTCTCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAGAGCCCTAGGTTTCCCTTCT
TCAGCCCTGTAAATTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCGAGTAACAT
CCACCATATAGAACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

CCACACGCGTCGCGCCGCGCGCTGCGTCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
CCGGGGTGCAGGAGCCGACATGCGCCCGCTTCTCGGCCCTCTTCTGGTCTTCGCCGGCTGCAC
CTTCGCCCTTGTAATTGCTGTGCAGCGGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
AGGCTGGAGGCGAGGTGCTGTGGTTCCTCCGACTGGCAGAGCTCGGGGAGCTCTCTGAG
GTCCTTCGAGAGTACCGGAAGGAGCACAGGCCCTACGTGTTCTCTGCTCTTCGCGCGCCTA
CCTCTACAAACAGGGCTTTGCCATCCCCGCTCCAGCTTCTCTGAATGTTTTAGCTGGTGCC
TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT
GGCCCTGCTGCAGAGAAAGGTGGAGGAGACGAAACAGCTTGGTTTTTTTCTTATTGTTTT
TGAGACTTTTCCCATACGACCAAACTGGTTCTTGAACCTCTCGGCCCAACTTCTGAACAT
CCCATCTGTGAGTTCTTCTCTCAGTTCTTATCGCGTTTGATCCCATATAATTCTCATCTGTGT
GCAGACAGGGTCCATCTGTCAACCTTAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG
TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCTCATTAAAAAATTT
AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
CACATGAATCTGGATTTTCTGTTTGCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
TGTGGTCTCTAAAGCCCTCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGATTACATCAGGT
TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCCTCTAGAAAAATGCTGTTTGT
GGCCGGGCGCGGTGGCTCACGCCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
ACAAGGTCTAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
ACAAAAATTAGCCAGGCGTGGTGGCAGGCAGCTGTAATCCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATTGCTTGAACCAAGGTGGCAGGTTGCAATAGCCAAGATCACACCAGTGCAT
CCAGCCTGGGTGATAGGTGAGACACTGCTTTCAG

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR
 KEHQAYVFLLFCGAYLYKQGFAIPGSSFLNLVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGQQLVVSYPDKVALLQRKVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
 TAGGAAAATAAATTGGGATTTTATATTGGAAGACATGGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTGGAGGAAGAGATTC
 AGCATTTTTTTGTGCCAGTACCCTGAGGCGACAGAAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTTCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCCTGTTTTCACTCACCTGCCATTTCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCCTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCACTCTGCGAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCGAGTTGAAAGGGGAAAAATAAAACAAAAACGATGAAACTGCAAAA

MDLAANEISIDKLSETVDLVRQTHGQCGMSEKATEKFIQRLLEKNEPORPPPPQYPLLI VVY
KVLATLGLILLTAYFVIQPFSLAPEPVLSGAHTWRSLIHHIRLMSLP IAKKYMSENKG VFL
HGGDEDRPFPDFDPFWNTNDCQESEFIPANCTGCAQKHLKVM LLEDAPRKFERLHPLV IKT
GKPLLEEEIQHFLCQYPEATEGFESEGGFFAKWRRCFERWFFPPYPWRRLNRSQMLRELFPV
THLFPFKDASLNKCSFLHPEFVGSGMKHMKPDLFI ISGSEAMLQLIPPFQCRRHCSVAMP
IEPQGVYDVTTHWKVYVIARGVQPLVICDGTAFSEL

CCACGGTGTCCGTTCTTCGCCCGGGCGGCAGCTGTCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGTCTGCCAACGAGATCAGCATTTATGACAAACTTTAGAGACTGTTG
ATTTGGTGAGACAGACCGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCTCTCCTTATAGT
TGTGTTAAGGTTCTGC AACCTTGGGATTTAATCTTGCTACTGCTACTTTGTGATTCAAC
CTTTACGCCCATTAGCAACCTGAGCCAGTGCCTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGTCCTCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTGTGGTGTG
 CCACCTGGTGGCCAGCGTCTAGACCGTGCCTATGAGCCGCTGGGGCTGCAGTGGGACTGGCC
 CTCCTCGCCACCCACCAATTGCGAGCCCACTTCTTTGAAGACTTCCAGGCTTTTGTGGCA
 CACCCGAATGGCGCCACTATCGACAACAGGTACAGCCAACCATGCCAGTCCGACTTCGAATG
 GACACGATATGCTAAGAGCCACGACCTTATGTAGGTTTCTGGAATGCTGCTATGATCATGTCT
 TATGAGTATGGGACGCGGCCACTGGAGCGCGCCAGAGTGGCTCGGGCTCTCCAGGAGC
 TGGTGTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGCTACGCTACACGGCCAGTGCTG
 AAGCAGCAGGCAACGCACTCCATGGCCCTGCTGCACTGGGGGGCTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGGCTTGGCGCTGAGGGACACTCCATCCCCCTGGAATCTGCCA
 GCGCCGAGACATATTCAGCATGCGCTGGAAGTGTGTGCCAACATCACTTCGACCCCTCAC
 CTGGAAGCGCAGCGCTCTCCGAGACAATCTGGGTGAGTTCCTTCGACACCCACGAGGAGCG
 CTCACTGCCCTCTGGCAGTGACCAAGAGGCCAAAGTGAGCACCCCGAGTTCGTGAGG
 AGGACCGAGCTCGGCGAGGACGAGCTGGCTGAGCTGAGAGCCCCGATGGAGGCGCAGAACTG
 GATGAGCAGCGTGAGAAGCTGGTGTCTGCGCCGAGTGGCAGCTGGTGACGGTAGTGGCGGT
 GGTCCCGAGGGTGTGGAGGTACCCACACAGAATGTATATCTACGATGCGACGACTGAGC
 GCGTGGAAACCGAGGAGGGCATCGGCTATGATTTCCGGCGCCACTGGCCGAGCTGCGTGTG
 GTCCACCTGTGGCGCTTCAACCTGCGCGCTTACGACTTGAGCTCTCTTTATCGATCAGGC
 CAACTACTTCTCTCACTTCCATGCAAGGTGGGCGACGACCCGCTCTCACTCTTACGACAGA
 CTCGAGAGCCCGAGCTGGGCCCCATCCCAACCCATACCCAGGTACGGAACAGGGTATCTCTG
 TGGCTCTCTGGCGCTACGGCCCTCTCAAGGCTACCTACAGCTGAGTCTCCCGCAGGAGAT
 GCTGCGTGTCTCAGGCCCTTACCCAGAAATGGGTACAGCTGAGATATCAATCTGAGGATCT
 TGATGCAACTCAACACCATGTGGGGGGGACCTACAGTACCTGTCTCAGTACCTGAGTCTC
 CCCTGGGTCTGACGAGTACGCTGCCCAACCCCTGGAGCTCAGCAACCCAGGCGTCTTCCG
 GGACTGTCTAAGCCCATCGGTGTGGTGAGAACCCCAAGCATGCCCGACTCTGTGAGGAGAAGT
 ATGAAGCTTTGAGGACCCAGCAGGGACCATTGACAAGTTCCACTATGGCACCCACTACTCC
 AATGACGAGCGGTGTGATGACTACCTCATCCGCTGGAGCCCTCACTCTCCCTGACGCTCCA
 GCTGCAAGTGGCCGCTTTGACTGCTCCGACCGGAGTTCACCTCGGTGGCGGCGAGCGTGGC
 AGGCAGCCTTGAGAGCCCTGCGGATGTGAAGGAGCTCATCCCGAATCTTCTACTTTCTCT
 GACTTCTTGGAGAACAGAACCGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGGCGATGTGGTGCTACCCCGTGGGCGAGCTCTCTGAGGACTTCATCCAGCAGCGCCG
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCGCGAGGAGGCCCTCAATGTCTTCTATTACTGCACTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCAGACTCCCTGTGCACTGCTGAAGGAGCCACATCCAATCGGCTCTCA
 GCTGAGGAAGCAGCCCATCGCCTTGCACGCTTGGACACTAACTCCACTAGCATCTTCCAGCA
 CCTGGACGAACTCAAGGCATTTCTCGCAGAGGTGACTGTGAGTGGCCGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAAGTCTCAGCAAGAGCCCC
 ACCATGGGCGAGCCACAAGACCGCAGCGACTGTGAGTGGCCCCGTGGGTGCCAGGCACTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAGCTGCTATTACGCGGTGGCACTGGG
 ATGGCGATTCGGGTGCTGCTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGGCTTGCAGTGGACACTGTGGCATCTACCTCATTCAGGCTCCCG
 GGACACCACTGCTGCTGTGGCGGCTCCTGCATCAGGGTGGTGTGTGAGTGGCCTGGCAG
 CAAAGCCTGTGCAAGTGTGTGTATGGGCAATGGGGCTGCAGTGAAGTGTGTGGCCATCAGCAT
 GAACCTGACATGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATCACTGATGACCGCG
 CGGACAGTTTGTAGCGGCACTACGGCTCTGGGTGCCACATTCCTTGGACCTATTTCCACC
 TGGCATTTGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAAGCTTTCGGGGC
 CAGGTCACTCTCTTGACCTGTATTGAGTCAATGGGAAGTTGGGGGCTTCACTGCCCT
 GGCAGAGCAGCTCAAGGCTGACGGTGACAGGAGCTTTGTGTTGCTGGGCGACCGCCAGT
 GCGCCCTGACATCTCTCAAGCTAAACACACTGCTCCCGCGCCGCGCTCCCTTGGCCATGAAG
 GTGGCCATCCGACGCTGGCGCTGACCAAGAGCGCAGCCAGTGGTGGGCTGGAGGA
 TGGCAAGCTCATCTGGTGGTGGCGGGGCGAGCCCTGTAGGTGGCGAGCAGGAGTTCCGCG
 GGAAGCTGTGGCGGTCTCTCGCGCGCATCTCCAGGTCTCTCGGAGAGACGGAATAACAG
 CCTACTGAGGCGCGCTGAAGCTGGCCAGTCCGGCTGCTCGGGCCCCGCCCCGCGAGGCTGTG
 GCCCGGAGGCCCGCCAGGAAGTGGCGGGGAACACCCGGGTGGGCGAGGCGGCTG
 GCGGGGCCAACCTTCCCAAGCTCAGGAGATTGGCGGGCGATGTTACCCCTCAGGAGTTGGCG
 GCGCGAAGTTCGCCCTTCCGCGCTGAGGGCGCCCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSAETYSRMRLKLVNP
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLEVTQNVFYFDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPPTLDLSNPAVFRDLSPKIGVVPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLES PADVKELIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVLPWPWASSPEDFIQQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAABEALNVFYCYTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDNTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLISGSRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAVS
 CVAISTELDMAVSGSEDGTVIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSA
 WERPGAQVITYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCCACCTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAATCTATGGGGTCTGGGGCTCTTC
 TGGACCTTAAC TGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGGCATTTGGAGCCCTCATCCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTGGAGTATATTGACCACAAGCTCAGAGGAGTG CAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTTCATGCTACTCATGCGAAACATTGT CAGGGTGGTCGTCTGGACAAAGTCACAGA
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGTCTGTCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCCTATGT CATCGCCAGCGGCTTCTTCAGCGT
 TTTCGGCATGTGTGGGACACGCTCTTCCTCTGCTTCCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCAACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACCTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTGTTAACCT

FIGURE 25

RTGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLGF
WTLNWWLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVGGVGVLSFFFFSGRIPLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKK
EAPPDNKKRKK

0000727-21201

FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGCT
 GGCT**ATG**TTCGTGTCGGATTTCCGCAAAGAGTTCACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTTGTTTC
 CAGTGTGACCACTGCAATATACGCTGGTTCAGTTCCTGGGTGGCAAGAACTTGAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGCATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTC
 AGGCCATGGACATCTCCTTGAAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGCGTGACACTTTCAGCATTCATTTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACCTCGCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTGATGCTGTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCCTTGTGTGTCGACAAAGAACGGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCAGATGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAACCTGGCTTTCATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDITFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDSGDSEPSEKRTLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLYQHWLSLHDSLNTSYTAARFKLWSVHGQKR
LQEFADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFYCYSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNFDSLVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCGGATTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGGATACACAGAAAAACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAAACGAAAGAGACAGTTTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGTTTTAACAAATT
 GAGTAAAGTACGCTCCGGTCAAC**ATGGT**GACAGCCGCCCTGGGTCCCGCTCTGGGCAGCGCTC
 CTGCTCTTTTCTCTGTATGTGTGAGATCCGTATGGTGGAGCTCACTTTGACAGAGTCTGGC
 CAGCGGCTGCCAACCGGTGCTGTACTCTGAGGACCCCTGGATCCTGCCATGTATCTCTCAG
 CCTCTTCTCCGGCCGCCCCACGCCCTGCCCTGAGATCAGACCTACATTAATATCACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCCTGCCAGGGTACATGGCCAGGGAGGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGCGAGCAAGGCTGACAAGGGGAGATGGGCAGCCCGG
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCCTTCTCAGTGGCCCGCAAGACGGCCCTGCACAGC
 GGGCAGGACTTCCAGACGCTGCTCTTCAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACCGCCAGTTTGTCTGCTCCCTGCTGGCATCTACTTCTTCAGCCCAATGTGTC
 ACAGCTGGAATTACAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTGATC
 CTGTACGGCGCAGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGCG
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAAGCCGACGGCCGAGAAAGCCCATCTACAGCA
 ACGACTTCGACACCTACATCACTTCAAGCGGCCACTCATCAAGGCCGAGGAGCACT**GA**GGG
 CCTCTGGGCCACCCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTCGAGGGCTCAG
 TTTTGACTGCTGTGAAGCGGAAGGCCAGGGAGGTTCCCGGGGACCTTGGCATTCTGGGGAGA
 CCCTGCTTCTATCTTGGCTGCCATCATCCCTCCCAGCCTATTTCTGTCTCCTCTCTCTCTCT
 TGGACCTTTTAAAGAAGCTTGCTAACTTAATATTCTAGAACCTTCCAGCCTCGTAGCC
 AGCACTTCTCAAACCTTGGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATCGAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCCGTGGGTGATGCTG
 ATGGGGTCACTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCTCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCT
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCTACTGC
 AACCTCTGCCTCCCGGGTTCAAGCGATTCTTCTGCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGGCGCTGCTACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCAACATA
 TTGGCCAGGCTGGCTTTGAACCTCTGACTTCAAGTGAGCCACCCGCTCGGCCCTCTCAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAAATCCAACATTTCTTAAATTTCTCTCAT
 CCTCTCAGGGGCTCCCGTGTCTATGTTCTCTTTACCCCTTCCCTCTTCTCTTGTCTCAGGCC
 TGCACCACTGCAGCCACCGTTTCAATTTATCTATTCAATTAACACTGAGCACTCACTCTGTGCT
 GGGTCCCGGGAAGGGTGAGGGGGTCAAGACAGGCCCTGCCCTGCCCTCAGTCACTGGCCCA
 GTCCAGCCCAAGCGGGGAGAGATGTGTACATAGGTTTAAAGCAGCCAGCCAGACTCATGGGG
 GCCTGTGTTCTGGGTGTTCAAGTGCTGCTGGTCTTCCATTACCACTGCTGCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGCGAGGGGAGGTTATCTCTTCCCGTTCTCTATCCACTCGCCAG
 TGCTCATCGTTACAGCAAAACCCAGGGGGCTTGGCCAGGTCAAGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCAATTTGGGGGGTGAAGTGGCCCCGAAGAAATGAACCCACACCCA
 TAGCTCTCCCCACAGCTGATACGGCATCTTGCAGAGAAGACTTGCCTCTCTCACTGGGATCC
 CTTCCTGCTCTCTCCAGGGCTCTGCCAGGGCTTGTCTCAGTCCCTTCTCCACCAAGTCACTCT
 GAACCTTCGTTTCCCGAGGCTTCCAGTCTGCCCTGAGCACTGATGTCTGTCCCCAGGTGCT
 CTCTGCCCCCTCATGCCCTCTCAACGGCCAGTGCCCCGACTCTCCAGGCTTTTACAAGGTG
 CTAAAGCCCGGGTGGGCAAGCTCTCGTCTCAGAGCCCTCTCCGGCTGGTGTGCTGCCCTTAC
 AAACACCTGCAGGAGAAGGGCCACGGAAGCCCTCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAGAGGAGGACCTCAGGCTTCCGTTTCTTTCCAGGGTGGGTGGGCTGGCTGGT
 GTTCCCTAGCCTTCCAACCCAGGTGGCTGCCCTTCTCCCCAGAGGGGAGGCGGCTCCCG
 CCATTGTGCTCATGAGTCTGGGGCTGAGGTGCCCGGGGGGTGATCTCTGGTGCTCAC
 AGCCGAGGGGAGCCGTGGCTTCATGGCCAGATGACGGAAACAGGTTCTGACCAAGTGCCAGGA
 AGACCTGTGCTATAAACACCCCTGCCTGATCTCGCTGCTGACCCGCCACGCGCTGCC
 GTCCAGCATGATTAAGAATGCTGTCTCTTGGAAAAA

0999727.11901

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDGDPGPMGLPGYMGREGPQGEPPQGSKGDKGEMGSPGAPCQKR
FAFSVGRKTALHSGEDFQTLLEFVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSPERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCACTTGCTTCGGGACCCAGGACCCCCTCGGGCCCCGACCCGCCAGGAAAGACTG
 AGGCCCGCGGCTGCCCGCCCGGCTCCTGCGCCGCGCGGCTCCCGGGACAGAAAGATGTG
 CTCACAGGTCCCTTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGACGG
 GCTGCCCATCCGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGCTTTTGAGAACGGCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGGCTGCCGGGCTGCAGCTCCTGGACCTGTGCAC
 AGAACAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACTCAGCAACCTG
 GACCTGACGGCCAACAGGCTGCATGAAATCACC AATGAGACCTTCCGTGGCTGCGGCGCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGAG
 AGGGGCTCTTACGCGCTTGGCGAACCTCCAGCAGCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCTCGCGCTGGCCGGCAACAC
 CCGCATTGGCCAGCTGCGGCGCGAGGACCTGCGCGGCTGGCTGCCCTGACGAGCTGGATG
 TGAGCAACCTAAGCCTGACAGGCTGCTGCGCAGCTCTCGGGCTCTTCCCCGCTGCGG
 CTGTGCGAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCTG
 GGTGCGGAGAGCCACGTCACTGCGGCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTAGCCGCACTTGGCTGCCAGCCACACC
 ACCACAGCCAGTGCCCGCACCGACGAGGCCGTGGTGGGGAGCCAGCCTTGTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCCAGCCCGCTTCCA
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGTGTGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACACGCTCCTGACCTGGGCATCGAGCCGGTGAAGCCCTACCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGGCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTGCTG
 AGTACACGGTCAACAGCTGCGGCGCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG
 CCGGGCGGGTGCCGAGGCGGAGGAGGCTGCGGGGAGGCCATACACCCCCAGCCGTCCA
 CTCCAACACGCCCCAGTCAGCCAGGCCCGGAGGGCAACCTGCCGCTCCTATTGCGCCCG
 CCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGCGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCT
 GGAACCTGGAGGAGTGAAGGCTCCCTTGGAGCCAGGCCGGAAGGCAACAGAGGGCGGTGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCCT
 CAGTACCCCTCCAGCAGAAAGCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCGG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCTCCTGCTGCCACACGTAAGTTCTCAGTCC
 CAACTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCGAAGC
 CGAGTGCTATGAGGACAGTGTCCGCGCTGCCCTCCGCAACGTGCACTCCTGGGACGCGG
 GGCCTTGCCATGTGTGTGTAACGATGCCTGGGTCTGCTGGGCTCTCCCACTCAGGCGGA
 CCTGGGGGCGAGTGAAGGAAGCTCCGGAAGAGCAGAGGAGAGCGGGTAGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATTTATAAGAGATCCTTTCCATTTATTCTG
 GGAAGATGTTTTTCAAATCAGAGACAAGGACTTTGGTTTTGTAAGACAAAGATGATATG
 AAGGCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAA

MCSRVP LLLPL LLL L L L L L A L G P G V Q G C P S G C Q C S Q P Q V T F C T A R Q G T T V P R D V P D T V G L Y V F E N
G I T M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R
R L E R L Y L G K N R I R H I Q P G A F D T L D R L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P
G I L T A N V E A L R I A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G
N T R I A Q L R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A R N P F N C V C P L S W F G
P W V R E S H V T L A S P E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S
S S L A P T W L S P T A P A T E A P S P S T A P T V G P V P Q P D C P P S T C L N G G T C H L G T R H H L A C L C P E
G T T G L Y C S Q M Q G V T R P S P T P V T P P R S L R L I E I P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L
F Y N L S G P D K R L G L T R L P A S L A E Y T V T Q L R P N A T Y S C A Y P G P G R V P E E A C C G E A H T P P A
V H S N H A P V T Q A R E G N L P L L I A P A L A V L L A A L A V G A Y C V R R G R A M A A A Q K G Q V G P G A G
P L E L E G V K V P L E P G P K A T E G G E A L P S G S E C E V P L M G F F G P G L O S P L H A K Y P I

FIGURE 33

GAATCATCCACGACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTCATATGAGGAAATAAGTGGTAAAAATCCTTGGAAATACATGAGACTCATCAG
 AAGCAATTTACATATTTTGTAGTATGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAGGGAACTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGACGCCACACGACACTGGATTATCCTATAACCTCCTTTTCTCACTCAGAGCTTCAGA
 TTTTCATTCTGTCTCAAACTGAGAGTTTTGATTCTATGCCATTAACAGAATTCACAGCTGG
 ATCTCAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTTTGTCTTAATACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGCTCAGGATTTAGATCTTTCTTTTAACTGACT
 TGACACCATGCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGTGTGA
 GTGGGGCAAAAAATCAAAAATCAGATTTCCAGAAAATTGTCTCATCTGCATTAATACTGTG
 TTCTTAGGATTCAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCACTTAAACACAAC
 AAAACTGCACATTTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGCTGATGGAATCA
 AGACTTCAAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAAATTTGAAGTTATGAA
 ATGCAACGAAATCTTAGTTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAGGTTGA
 TTTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTTGGCATACATCAGTGGGAACCT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC
 TCAAAATCTGTAATGAGAACTATAAAATGGAGCATGTACATTCAGAGTGTTTTACATTC
 ACAGGATAAAATCTTATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAATG
 CACAAATGGCCACACATGCTTTTCCGAAATTCCTACGAAATTTCAAATTTAAATTTTGGC
 AATTAATATCTTAAACAGACGAGTTGTTTAAAGAAGTATCCAAGTCCCTCCTTCAAAAATCT
 CATTTTGAATGGCAATAAATCGAGACACTTTCTTTAGTAGTTGCTTGTCTAACAACACAC
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAAATTTGCTCA
 TGGCCAGAAAATCTGGTCAATATGAATCTGTATCAATAAATTTGCTGATTTCTGTCTCAG
 GTGCTTGCCCAAAAGTATTCAAATCTTGACCTAAATAAACAATCCAAATCCAAATCTGACCT
 AAGAGACTATTCATCTGATGGCCTTACGAGAAGTAAATATTCGATTTAAATTTTCTAAGCTAT
 CTCCCTGGATCGAGTCATTTAGTAGACTTTCAGTTCTGAACATTTGAAATGAACTCTTCTTT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTAAACACTCTAAATGCGGGAAGAA
 ATCCATTTCCCGTGTACCTGTGAATTAATAAATTTTCATTCAGCTTGAACATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGATTCATACACCTGTGAATACCTTTAAACCTAATGGGGAACATG
 GTTAAAGACGTTCTATCTCCACGAATATCTTGCAACACAGCTCTGTGATTGTACACATTG
 TGGTTTATATGCTAGTTCTGGGGTTGGCTGTGGCTTTCTGTCTCCACTTTGATCTGTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCAGAGGTTAGGAAAAACCCCA
 AGAACCACTCAAGAGAAAATGCCGATTCACGCATTTTATTCATACAGTGAACATGATTTCT
 TGTGGGTGAAGAATGAATTTGATCCCAATCTAGAGAAGGAAGATGTTTCTATCTGATTTGC
 CTTTATGAAAGCTACTTTGACCTGGCAAAAGCATTTAGTGAATAATTTGAAGCTTCAATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCAACCTTTGTCCAGATGAGTGGTGCCATTT
 ATGAATTTCTACTTTGGCCACCAATCTCTCCATGAAAATTCAGATCATATAAATTTCTATTC
 TTACTGGAACCCATTCCTATTTGCAATTTCCACAGGATCATAAATCTGAAAGCTCTCTCT
 GGAAAAAAGGCATACTTTGGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTCTGGGC
 ACCCTTCGAGCTGCTATTAATGTTAATGTATAGCCACAGAGAAATGTATGAATCGCAGACA
 TTACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT
 ATAAATTTCCACAGTCTTGGGAAATTTGGGGACCACATACACTGTTGGGATGTACATTTGATA
 CAACCTTTATGATGGCAATTTGACAAATTTTATTAATAAATAAAGGTTATTTCCCTTTCTA
 TCAAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAAACCTTCAAGATTTTATAAGG
 GCTTATGGAATAAGGTTGTTCTCCAGGATTTTATAATGATAAAAAATGGGCGAGGTCG
 AGTGGCTCCTCTTGTGAATCCAGCAGCTATGGGAGGCCAAGGTGGGTGAGCCACGAGGTC
 GAGATGGAGACCATCTGGCCCAACATGGTGAACCCCTGCTCTACTATAAAATACAAAAATTA
 GCTGGGCGTGATGTTGCACGCTGTAGTCCAGCTACTTGGGAGGCTGAGGAGGAGGAATCG
 CTTGAACCCGGGAGGTGGCAGTTGCAAGTGAGCTGAGCTGAGCCACTGCACTCCAGCTGTG
 GACAGAGCGAGACTTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAACATCC
 TCAATGGCCACAAAAATAAGGCTAAATTCATAAATTTATAGTAAATGTAATATAATATTA
 CATGCCACTAAAAAAGATAAGGTAGCTGTATTTTCTGGTATGAAAAAACAATATAATAT
 GTTATAAATCTTAGTTGGTGGCAAACTAATTTGGTTTTGGCATTTGAAATGGCAATTTGAA
 ATAAAGTGTAAAGAAATCTATACAGATGTAGTAACAGTGGTTGGGTCTGGGAGGTTGGA
 TTACAGGAGCAATTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATGTTTGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAGATAGTTTTACAGCT

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FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHVSVKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNfANNILTDELfKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLQHKNDENCsWPETVvNMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMAReLNIAfNfLTDLPgCSHfSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIvVIMLVGLAVAFCLHFDLPWYLRMLGQCTQTWHRV
RKtTQEQlKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSfIEKSYKSIFVLSPNFVQNEWCHYEFYFAHhNLFHENSdHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVlATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCCCTCGGAGGGGTGCGCCGGGAAAAG
 GAGGGAAGAAAGGAAGGGCGGGGCGGCCCGCTGCGCCGCGCCCGCGCTTCTGCGCGCCCTGTCCGCGCCCGGCG
 CCAGCCCGACGCCAGCCCGCGGGCGGTACACGCGCAGCCAGCGCGCCGCTTCCGCGGCCAAGCGCGCGCCGT
 CTCTGCTGTGCCCTGCGCCCTTGCCCGCGCCAGCTTCTGCGCCGCGAGCCCGCGCGCCCGCGCGCGGTGACCGCTGA
 CCTCGCCTGGGGCGGGGCGGAGCAGGCA**ATGT**CCCCCGCGGGACCGCTACCCAGCGCTGGCCCTGCTGCTC
 CTGGCAGTGACCCCTGGCCGGGTGCGAGCCGAGGGCGAGCCCTCGAGGACCTGATTATTACGGGCGAGGAGAT
 CTGGAGCCGGGAGCCCTACTACGCGCGCCCGGAGCCGAGCTCGAGACCTTCTCTCCGCGCCTGCTCGCGGGGAT
 CCGGGGAGGAGTGGGAGCGCGCCCGCGAGGAGCCAGGCGGCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCC
 AAGAGSGAAGAGTCCGCTCCGGAGCCGCTCCACCAAGGTAAACACAGCAACAAAAGATTATGAGAAGCAAGAG
 CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCCGTGTGGCCGTGAAGATGTGAGAGAGAGTTGCCACCTC
 TTGCTCTGGAAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCTTGGGGCA
 CATCGAGGGAAGACTCAACATCCAGCGGGCATTAAATAAGAAATGATTTTATGACGGAGCGTGGTGGCGGGGAAG
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCTGACCAGATTCACTGGTGTATCACTCAAGGGA
 GGAACCTCCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTCATGGTGAAGCAATGACAGCCACACGTGGGT
 ACTGTTAAGAATGGATCTGGAGACATGATATTGAGGGAACAGTGAAGAGGATCCCTGTTCTCAATGAGCT
 ACCCGTCCCATGTGTGCCCGCTACATCCGCATAAACCCCTCAGTCTGTGTTGATAATGGGAGCATGTCATGA
 GAATGGAGATCCTGGGCTGCCACTGCCAGATCTTAATAATTATTATCACCGCCGGAGCAGATGACCAACCAT
 GATGACCTGGATTTAAGCACCAACAATATAAGGAAATCGCCAGTTGATGAAGTTGTGAATGAAATGTGTCC
 CAATATCACAGAAATTACAACATTTGAAAAAGGCCACAGGGGCTGAAGCTGTATGCTGTGGAGATCTCAGATC
 ACCCTGGGGAGCATGAAGTGGGAGCCGAGTTCACACTACATCGCGGGGCGCCACGGCAATGAGTGTCTGGGCG
 CGGAGAGTGTGCTGCTGCTGGTGAGTGTCTGTGTGAGGAGTACTTGCGCCGGAATGCGCGCATGCTCCACCT
 GGTGAGAGGAGCGGAGATTACCGTCTCCCTCCCTCAACCCGATGGCTACGAGAGGCTACGAAAGGGCGGT
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTCTCATTATTA
 AACACGCTGCTCTGGGAGGCGAGGATCGACAGAATGTCCCGAGGAAGTTCCCAATCATATATTGCAATCCC
 TGAGTGGTTCTCTCGGAAATGCGACGGTGGCTGCCGAGACCAGAGCAGTCAATGCCCTGGATGGAAAAATCCC
 CTTTGTGTGGGCGCAACCTGCAGGGCGCGGAGCTGGTGGTGGCGTATCCCTAGCAGCTGGTGGCGGTCCGCC
 TGGAGAGCGCAGGAACACACCCCGACCCCGATGACCACGCTGTCCGCTGGCTGGCCCTACTCCTATGCCTCCAC
 ACACCGCCTCATGACAGAGCGCCCGGAGGAGGTGTGCCACAGGAGGACTTCAGAGAGGAGGCGGCTGTCA
 ATGGGGCTCCTGGCACACCGCTGCTGGAAGTCTGAACAGATTTCAGCTACCTTCATCAAACTGCTTCCAACTG
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCCGAGGATGGGGAATACACCGGAATC
 TCTGATCCTGTTACATGGAGAGGTTATCTGTGGCATTAAGGCTTGGTGAAGATTCACATGGAAGAAGAAATCC
 CAACGCCATTAATCTCGGTAGAAGGCATTAACCATGACATCCGAACGCAACGATGGGGAATTACTGCGCCCTC
 CTGAAGCCCTGGAGAGTATGTGTGCTCAGGCAAAAGCCGAAGGTTTCACTGTCATCCACAGAAGCTGTATGGTGG
 CTATGACATGGGGGCCACAGGTGTGACTTCACATTAGCAAAACCAACATGGCCAGGATCCGAGAGATCATCG
 AGAAGTTTGGGAAGCCCGCTCAGCTGCCAGCCAGGCGCGCTGAAGCTGCGGGGGCGGAAGGAGCAGCGCT
 GGG**CGA**CCCTCCTGGGCCCTTGAGACTGCTTGGGACCCATGCAAAATTAACCAACCTGGTAGTAGCTCCATAG
 TGGACTCACTCACTGTTGTTTCCCTGTAATTAAGAAGTGGCTGGAAGAGAGGGTGCATGTTGAGGCGAGGCTCC
 CAAAGGGAAGGCTGGAGGCTGAGGCTGTTTCTTTCTTCTTGTGCCATTTATGCCAAATTACTTGGACGAGCA
 CAGAGAAAAGCTGATGGGATGAGAGAACTCAGCAAGCCAACTGGGAATTAGAGAGAGAAGGAGAAGGAGGG
 GAGCTCTGCTCGTTTCAGAGCCTCTGGCTGCATAGAAAAGGATTCTGGTGTCTCCCTGTTTGCCTGGCAGCAAG
 GTTCCACGTGTGTTTGCATTTGGCACGCTAAATTTGAGCATTTCCCGAGTGGGCTGCCCAATGTTACCA
 TTTGAGATGCTCCCGGCGCTCTAAGAGAATCCACCTCTCTGGCCCTGGGACATTGCAAGCTGCTACAAATAA
 ATTCTGTGTTCTTTTGACAAAGGCTCATTGCCAAATGACATCAGTGAGCCCTTGAATCTGTTTGAATCTGCT
 TTTTCAACAAAGAGGTGTGTTTCAGAAAAGGAGAGAGGCTGAGATCATCAGGAGATTGTTGGGCGAGCAAGCA
 GATTAGGCTTCTTGGACAAATTTCTGGTCCATAAACCAACCCCAAAGTCCCTGCTGATCAGCAGTCCCTGGAGGTT
 CCCCAGGTAGGAGGAGCCAGAGTGCACCGCTTCTGAAGGGCCAGAAATTTAGCCTGGATCTCCTCTTTTAC
 CTGCTAGGACTGGAAAGAGCCAGAAGTGGGTGGCTGAAGCCCTCTCTGCTGAGGATGGGCCCTGTGTG
 GAATTGAGTGCTCATGGTTGGGCTCATATCAGCTGGGAGTTATTTTGTATGTAGAATGCCAGATGCTTCCA
 GATTAGGCTAAATGTAATGAAACCTCTTAGGATATCTGTGGAGCATCAGTTTGGGAAGATTTGAATTAAT
 CTTGCAAGAAAAAGTATGTCTCACTTTTGTGTAATGTTGCTGCCTCATTGACCTGGGAAAAATGAAAAAAA
 AATAAGCAAAATGGTAAGCCCTTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPPDYGGQEIWSREPPYARPEPELETFSPLP
AGPGEEWERRPQEP RPPK R A T K P K K A P K R E K S A P E P P P G K H S N K K V M R T K S S E K A A N D D H S
V R V A R E D V R E S C P P L G L E T L K I T D F Q L H A S T V K R Y G L G A H R G R L N I Q A G I N E N D F Y D G A W C A
G R N D L Q Q W I E V D A R R L T R F T G V I T Q G R N S L W L S D W V T S Y K V M V S N D S H T W V T V K N G S G D M I F
E G N S E K E I P V L N E L P V P M V A R Y I R I N P Q S W F D N G S I C M R M E I L G C P L P D P N N Y Y H R R N E M T T
T D D L D F K H H N Y K E M R Q L M K V V N E M C P N I T R I Y N I G K S H Q G L K Y A V E I S D H P G E H E V G E P E F
H Y I A G A H G N E V L G R E L L L L V Q F V C Q E Y L A R N A R I V H L V E E T R I H V L P S L N P D G Y E K A Y E G G
S E L G G W S L G R W T H D G I D I N N N F P D L N T L L W E A E D R Q N V P R K V P N H Y I A I P E W F L S E N A T V A A
E T R A V I A W M E K I P F V L G G N L Q G G E L V V A Y P Y D L V R S P W K T Q E H T P T P D D H V F R W L A Y S Y A S T
H R L M T D A R R R V C H T E D F Q K E E G T V N G A S W H T V A G S L N D F S Y L H T N C F E L S I Y V G C D K Y P H E S
Q L P E E W E N N R E S L I V F M E Q V H R G I K G L V R D S H G K G I P N A I I S V E G I N H D I R T A N D G D Y W R L L
N P G E Y V V T A K A E G F T A S T K N C M V G Y D M G A T R C D F T L S K T N M A R I R E I M E K F G K Q P V S L P A R R
L K L R G R K R R Q R G

CTAAGAGGACAACTGAGAGGCTCGGCGCTCTCATTTCCTCTAGCCCTCTGTGTCTTCCTGGCCAAAGCTTCGAGGGG
TTCTCGGGCATCTGGGAGCTCCATTCCAGCGCCCGGCTTCAGCTCTTTCCTGGAGTGTTGACCTCCAGCTCCAGC
TTACGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCGAGCTAGGACGGGAGGTTCTGTCTCCCGAGTTTGT
TTCCAATTTCACCGGCTCCGGTAGTCAGCTGGGACCTGGCAGTGCTGTCTTCCTCCGCGACACACACCTTCTC
CGGTGGACAGAGTGGAACCGTTGGAATCCAGCTCATGTCTTCTTCAGAGTTTGGAGAAGAACTTTCAA
TGTGGAGGAATATGTCCRAATTAATAGTGTGTAGAAAGAAATCTTAAACCTTAAGCTTCGGAATGACATCAT
GGAGAAGGATACCTTTCTTACATGAAGTGGACTTCAGCTGTAGCAAGTAGAAGTGAAGGAGATGGAAAAAC
TGGTCATACAGCTGAGGAGGAGTTTGTGGGAAGCTCAGAAATTTGTACACAGCTGGAGGTGGAGATAGAAAT
ATGACTCTTCTGGTAGAGAAGCTTGAGACATGACAGAAAACAACTGTCTTGCCTTTCGGCGAGAAATCGTGGC
TCTGAGACCAAGCTGAAAGAGTTGTAGGCGCTTAAGATCAAACACCCCTGTGCACCTCTCTCCCACTC
CAGGGAGTGTGTCTAGTGGTGTGTGTGACATCGAGAACCCGTGTGGTTTTCAGCTCAACTGGAGAGGGTTT
TCTTATCTATATGGTCTTGGGGTGGAGTTACTCTCCCAAGCTCAAACAAAGGACTGTATTTGGGTGGCGCC
ATTGAATACAGATGGGAGACTGTTGGGATTTATAGACTGTACAAACACTGGATGATTGCTGTTATATTA
ATGCTCGAGAGTTGCGGATCACTTATGGCCAAAGTAGTGTGCACAGCATTTACAAACAAACACTGTAGCTTAAC
ATGTACAAACCGGGAAATTTGCCAGAGTTAACTGACCAACACAGATGCTGTGACTCAAACTCCCTTAA
TGCTGGCTATAAATACCGTTTCTATATGCTAATGTGTCTTGGCAAGATATGAACTTGTGTGTGGATGAGAATG
GATTGGGTTTATTTCTTAACTGAGGCCAGCTGTGAATGGTGATTAGAACTCAATGACACCACTCT
CAGGTGCTTAAACACTTGTATACCAAGCATATAAACCATCTGCTTTCACGGCTTCACTGGTATGTGGGGTGT
GTATGCCCGACTACTGTAAACACAGAACAGAAAGTTTACTACTATGACCAACCAAGGGAAGAG
GCAAACTAGACATGTATGCTATAGATGACGAGAAAGTGCAGAGCAATTAACATAAACCCCTTTGACCAAAAA
CTTTATGTCTATAACGATGGTACTCTCGAATTTATGCTTCTGTCTCGAGAGAACCGACTAAAGCTGTTTA
GGATGTAGGGTGAAGAGAAAAATTTGTTGAAGAAAATATGCTTCTCCACTTATAGATATCGAGGGGTGT
CTAAAGTGTGTCTTCTTTCGCAAAATGTTAGGTGCATAGTTTACCAACACTAGAGATCTAGGACATTTGCT
TGATTTGTGGAGTTCTCTTGGGAATCATCTGCGCTTCTCAGGCGCATTTGCAATAAAGTGTCTCTAGGGTGGGA
TTGTGAGAGTCTAGGGGCATCTGGGGCTGTAGGAAGCTACTGTGAGGAGCTTCACTAGAAGCCCTTAATTA
GGAATTAAGGAATTTAAACTCAGTAGGGGCTAGGAGTTCTTTGTCAGAAAATTTGCCCAATGACTAGTGC
CTCATCCATGTAGACCAACTAATTTCTTCATGCTCGGAGAAACCTGGGGAGCTAGTTAGTGAATATATATCT
GGAGCTCTCGAGGAGCAAAATCTCCAATTTTTTTTCCCTCACTGACATGCAAGTGGAAATGATGCTTGTATGTGG
CAGATAGTAATTTTGGCATCTTATATATCTACATCTGAAGAGTGCAGTTTATGAGAGAGGAGCCCTTTT
ATGCTAATTTGATCATGGCAATTAATCCGAGGAAGATCTGTAGATGAGGCACCTGCTTTTCTTTCTCTC
ATTGTCCACTTACATAAAGTCAGTAGAATTTCTTACTCTATAACTCTCTCCAAAGGAGCCTCAGAAGATAG
AACCAGCTTACTAACCAATTCACCCGCCCAACCCCTCTTCTACTGCTCACTTTAAAAAATTAATAGTTT
CTATGAACTGATCTAAGATTAGAAAAATTAATTTCTTTTAATTTGATATGAGCTTTTATACGATGCTCA
AGACTATAGAAAAATCTGATGGCAGTGACAAAGCTGTGACATTTATTTGTTATTAATAAGACCTTGGAGCAT
TGTGCAACTTATGAGTGTACAGTTGTGTGATGTAATTTTGGCTCTTTTAAGCTGGAACTGTGAAGAAAT
GAAATTTAAATTTTTTTTTCAGGACAGAGCTAGAAAAGCTATGAGAGTATCTAGTTAATCAGTGCAGTAGT
TGGAAACCTTCTGGTGTATGTGATGCTCTGTGCTTTGAATGACTTATCATCTGCTTTTCTCTATT
TCTCTTGATGTCAAGTCCGATCTATAGGATGGCAGTTTAAATGCTTTACTCCCCTTTTAAATTAATGAT
TAAATTTGCTTTGGAAAAAATAAAAAAATAAAAAA

FIGURE 38

MRPGLSFLLLALLFFLGLQAAGLDGVDGPPIPSPGGSFFPGVDSSSSFSSSSRSGSSSSRSLSGS
GGSVSQLFSNFTGSVDDRGTCQCQSVSLPDTTFPVDRVERLEFTAHVLSQKFELKSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESPGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKEKECEASKDQNTFPVHPPPTPGSCGH
GGVNVISKSPSVQNLNRGFSYLYGAWGRDYSPOHPNKGLYWVAPLNTDGRLLLEYRYLNTLD
DLLLYINARELRITYGGSGTAVYNNNNMYNMNTGNIARVNLTNTNTIAVTQILPNAAYNNR
FSYCNVAWQDIDFAVDENGLWVIYSTAEGNMVVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVGCVLYATRTMFAVNTTEEIFYYDTNTGKEGKGLDIVMHKMEQKVQSYNNPFDQKLYVYNDG
YLLNLYDLSVLQKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCCCATTTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

TC CGCATAGTAACTAAATCTCGGAAGAGCTCGAAGGAAGCTGTCTCCATCTTGTCGTGAT
CCCGTCTCTCTTGAGACTTCTGGAGATGCGGAGCGCTCTGGGGCTGTCCTCATGGCAGCT
GGATACCAATGTTTGTGTGGAAGTGCGCCCTGTTTGCATAGCCGATGCTCTCCATGTGGAAC
AACTCCACTGTAACTAGTATGATCTAGCATTTCTTGGCTTTGGGATGTGTGACATTG
TGTAATGTGTATACACGAAGTGAAGAACCACTGAATAAGATTCTCGATTTTGTGAGAATG
AGAAAGGTTGTGTCCCTTTGAAACATTTTGGTTGGCTATAAAGCTGTATACGTTTGTGCTTT
GGTTTGGCTATGTTCTATCTTCTCTCTCTTTACTAATGATCAAAAGTGAAGATGAGCAGTGA
TCTCTAGAGCTGCAGTGCACAAATGAATTTTGGTCTTTAAATTTGCTGCAGCAATGCAATTA
TTATTTGGGGCATTTTCATTTATCCAGGAAGCAATTTTCAACAGTGTGGTTTATGTAGGCAT
CGAGGTGGCTTTTGTTCATCCATCAATACTAGTCTTACTATTGATTTTGTGACATTCAT
GAATGAATTCGTGGGTTGAAAAAATGAAGAAAGGAAGCTCGAGATGTGTGTATGCAGCCTTGT
TATCAGCTACAGCTCGAATATPTCGTCTGTTTGTAGTGCTATGCTGCTGTTCTTTGTCTAT
TACACTCATCAGGCAGTGTGTTGCAGAAAACAAGCGGTTCACTCAGTGTGCACATGTCTCCTGT
CGTTGGTGCTCTGTGAATGTCTATAGCTGCCAAAAACGAAGATACACAAAGATCTGGTT
TGTTACAGCTGTTTCAGTAATACAGCTTACACAAATGTAATTCAGATGTGTCAGTATAGCCAA
GAACCGAAGAAACAAATGCAACCAAGCTACTAAAGCAATAATGGCTACGATACAAACAAGAC
TGTCCTCAGGAAGGAGGCGATCAGTCAGCGTGTGGCAGTCTCTCAAGGAATATAGGACTAAATC
TCTTTTGTGTGTGTATTTTATTCAGCATCGCATCTCAAAACAATGACAGGTTAATAAAA
CTGCATCTCAACAGATGATGAATCTACATTAATGAAGAATGTTGGAGCTAGAAGTGTGATG
ACTGGAGATGGGGACGATGTTCCAGCAGCTGTAGATAATGAAGAGGATGGTGCATCTACA
GTTATCTCTCTTCTTCACTTACATGCTTTTCTCGCTCACTTTATATCATGTAGACCTTACC
AACTGGTCCAGGATGAACCCCTCTCGTAGATGAAAGAGTGGTGCAGACAGCTGTCTGGGTA
AATCTCTTCCAGTGTGGATGGCATCGTCTGTGTAATGTTTGGACACTCTGGCCACCATTTGTC
TGACAAATCTCGATTGTTGACATGAGACTCTAGCATGAAGTCCCACCTTGATTATGCT
TTATTTGAAAACAGTATCCCAACTTTTGTAAAGTGTGTGATGTTTTGCTTCCCAGTAA
TCTCCAGTGTCTGCGATGAATAGATTTTACTGCTGTGATTTGTTTGTATTTCTTACCAA
GTGCATGTGATATGTGAAGTAGAATGAATTCGAGAGGAAAGTTTATGAATATGGTGATGAG
TAGTAAAGGTGGCCATATTGGGCTTATTTCTCTGCTCTATAGTGTGAATAGGAAGTAA
ACAAATTTGTTTGACTATTTTAAAAATTATATAGACCTTAAGCTGTTTGAACAAGATAAA
CGAAATGTATGGCTGCTTTTGAATAATTTGATGTGTGGCTGGCAGGATACGCAAAAGAC
ATGGTTTATTTTAAAAATTTAAACCAAGTCACTTAAATGCCAGTCTGTGAAAATCTTATA
AGGTTTACCCTTGATACGGAATTTACACAGGTGAAGGATGTTTGTGTCGAATAGTGTAGG
TTATGTGATGGAGGTGTCGGTACTAAATTTGAATACACAGTAAATAATCTTACTTGGGTAGA
TGGCTTTGCCAACAAAGTGAACCTGTTTGTGGTTGTTTAAACTCATGAATATGGGTGAGT
GGAAATTTTGGAACTCTGGAAGGATTAGACAAAGTTTGTGAAAAGGATAATCATGGTTAGA
ACAGAGTGTGTTAGATGTCATGTTTGAAGTTGATTTTGGGCCGACACGCTAGCTCACTCT
TGTGTTGTTTGGGAGTGTGTTGGGTTGGGTTGATTACTGTGACCGAGGAATCAGACCA
GCTTGGCACAAGTGAATCTTCTTATAAAAAATTAATCTGGCTTTGAGCCTATGCTTGTGCT
GAGCTCAGAGCGCTAGTGCAAGTCTGAGCCAGAGCAAGGTTGAGGTGAGCAAGTCA
GCTCAGCTCACTCTAGCTCAGCAGTCACTGAAATATATATATGTAATGTAATGTAAT
AGGCAAAATTTGACAGGGAAGGAAGTATCGAAATCCCTCTTTTGTAGTCTTACTTAT
ATAAAATCTAGTCCAGTCTCTCATTTAAAAAAATGAAGCACTGAAATACAGACTTAATA
CTCGAGATAGCTAAATAGGAATTTCAAGTTGGCCATAATAGCATCTCTCTGACATTTAA
AAATAAATTTCTATCAAAATACATGCATATTTGATTTACACCTCACTGTGATAATTAATGT
GATGTGGAATGCTGTGTGTCAGCATGACCATAAAACAGGTCAAGAAGTGTGAAGATGTTT
AGAATAAACTCTGCTTATAGTATATACACAGTCAAAAGATGTTTAAATGCTTTTGTAT
TTACTGCCATGTAATGAAATATATAGATTATTGTAACCTTTCAACCTGAAATCAAGAGT
ATGAGAGTTTAGTATTGTTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTCAACT
TCTCTTTTAAAAAATTTTAAATGTGAATGGAATGAATAACAAATCAGCTTAATTTCCCAACC
TTATCTGTGTGTAGACATTTGATTTCCACAATTTGATGTGCTGTGTTTACCTCTAAATTA
ATGAAATTCAGAGAAAAAATAAAAAA

MGSVLGLCSMASWIPCLGSGAPCLLRCCPCSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVPVPCNILVGKAVYRLCFGLAMFYLLSLLMTIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFPIPEGTFTTVWFVYVGMAGAFCFILQLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVKNLTLSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVTYSYSFHFMLFLASLIYIMTLTNWSRYEPSREMKSQWTAVVVKISSSWIGI
VLYVWTLVAPLVLTNRHFD

SCGAGAAAGAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAACAANTCCACGTAACTAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCGAATGGAAG
AACAACGAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTGTCCCTTGTAACATT
TGTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTGGTTTGGAGTATGTTCTATCTTCTCT
CTCTTTACTAATGATCAAAAGTGAAGAGTAGCAGTAGCTTACGAGTCGAGTGCACAAATGGAT
TTTGGTTCCTTAAATTTGCTGCAGCAATTGCAATTATATATGGGGC

FIGURE 43

GTTATTGTGAACCTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNTATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAACTAGATTGATCTATGCACCTT
TTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGAAGAACAACCT
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTGTCCCTTGTAAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCATGTTCTATCTTCTCTCTTTTA
CTAATGATCAAAGTGAAGAGTAGCATGTATCTTAGAGTCGAGTGCACAATGGATTTTGGTT
TCTTAATTTTGGCTGCAGCAATTGCAATTATTTATTTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTTCATCCTCATACACTAGT
CTTACTTATTGATTTTGCACATTTCATGGAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGCTTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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TGGGCGGCGCAGACGGCAGTGGTGTGCGCTCGATTGAGCTCGGGGTGGGGCGGGGCGGGCTCTCCAAT
 CGGAATGTGTGTGGCTGGAGCGAGCGAGCGCTGTGGCGAAGCAGCTGAGTGTGTCAGCAAGCGGCGAG
 TCTGTGTGAAGACAGATTAAAGAAACAACTTATTAACTGTCTATTACGAGGAGCGCCCGCGGGCTGTCCG
 ATCTCCCGCGGAACATTTGGCTCTCCCTCCAGCTCGGAGAGAGAGAAAGAACGCGAAAGCGCAATTAC
 CTGTTTTCACGAGTGGTGGACCACTGATCACTGCCCTCTCTGAATTTATCAGATATTTGATTATTAGCAGTGC
 CTCTGGTTGTCTGTGTACCGACACACCTGCAGAGGAGGCTGTGGCTCGCTTCCCTCGTCTTCAGCTCG
 TGGGCGAATCCCACTCTGTTTCAACTCTCCGCGAGGCGAGCAGAGCGAGAGTGTGCGAATTCGCGAGTG
 AAGAGGGAGCGAGGGAAGAAACAAAGCCAGACGCCAGCTTGGAGCTCCCGCATCCCAAGAGAGACAGAGT
 CAGCAAAAAAAGAAAGATGGGCGCCCCGAGCCTCTGCTGCTGTCTGTGTGCGCAACTGTGTTCTCTGTGTG
 TGGAGCTCTGGCCTCTCTGTGCGACCAACCGCTCGTAAGAGCAGGTTTCAGAGGAGCCGCGAGCAATCGGCCCA
 ACATCATCTCTGTGCTGCAGCGACGACAGGATGTGAGCTGGTTCATCGAGGTGTAAACAAGACCGGGCG
 ATCATGGAGAGCGGGGGGGCGCACTTCACTCAAGCCCTGTGACAGCAACCATGTGCTGCGCCCTCAGCCTCTCT
 CATCTCTACTGGCAAGTACGTCTCAACAACCAACCTACACCAACATGAGAACTGTCTCTCGCTCTCGTG
 AGGCACGACGACGAGGCGGCACCTTTGGCTGTACTCAATAGCACTGGCTACGCGACAGCTTCTCTGGGAAG
 TATTTTAATAACACGCTGTGTGGAAAGCGGGTGAAGAGAGAACCGGCTCGCACTCTCCAGGATTAOTCTCA
 CAGACCTCATCAACATACAGCTGAGCTTGTCTCCGACCTCAAGAGATGTACCGCCAGCGAGCGAGCTCTC
 ATGTGTCATAGCCATCGACGCCGCCCGCGCCCTGAGGATTAGCCGCCACAATTTATCGCCTCTCCCCAAAGC
 ATCTCAGACATCATCGCGCGAGCTACAACTACGGCGCCACCGCGCAACAACTGGATCATGGCTACACGGGG
 CCATGAAGCCCATCCACATGGAATCCCAACATGCTCTCAGCGGAAGCGCTGTGCAGACCCCTCATGTGTGGTGAG
 GACCTCTGGAGACATTATCAACATGCTGTGTGAGAGGGGCGACTGACAAACAGTCACTGTATACACCGC
 CGACACAGGTTTACCATCTCGGCACCTTTGGCTGGTGAAGGAAAGAAATCATGCATATGATTTGCATCAGGG
 TCCGGTTTCTAGTGTAGGGGGCCCAAGTGGAGCGCGCTGTGTAATCCCACTCTGCTCAAACTGACCTGT
 GCGCCCACTCATGGCAATTCGACAGCTGACATCTCTCGGATTTGAGCGGGAATTCATCTCAAGCTGCT
 GGAACAGAGCGCGCCGGTGAATCGTTTCACTTGAAGAAAGATGAGGTTCTCGCGGAGTCTTCTTGTGGTG
 AGAGAGAGAGAGCTGTCTACAAAGAGACATGACAGAGTGAGCGCCAGAGGAGAACTTGTGCCAAATGT
 AAGCGCTGGAAGCACTGTGTACGCTGCTGAGTACAGCGGGTGTGAGACGTGGGAAGAAGTGGAGTG
 TGTGGAGAGACGCGACGGGAAGCTGAACTGCAATGTGTCAGGGCGCCATCGGCTGTGGCGGCGACAGAGCC
 TCTCCAACTCTGTGCGGAGTCTACCGGCGAGGCGAGCGAGCTCGACCTGTGACGCGGCGACAGCAAGCT
 ASGCTGTGGCGGCGCGGAAATTAATCTCAAGAAAGTACAGGCGAGCTATGTCCCGAGTGTCTCATCTCGC
 TCAATGGCCATCAGAGTTGACCGCAGGCTGTACCACTAGGTAGGCTGGGTGTGCGCGCAGCCGCAAACTCA
 CCAAGCGCGCATCGGCAAGCGGCCCTTGAGGACAGAGATCAAGAACTGTGGGGACTTCAATGGCATGTGAGG
 TCTCCCGACTACTCAGCGGCCAACCCATTAAAGTACACATCTCGTGCTACTCTAGAGAGACACAGACTCCA
 GTGTGACTCGAATCTGACAGTCCCTCGAGCCTCGAAGAGCAACAAGTGCATCATGACACAGCAAGTTGAA
 CCTCGACGAACAAATTAAGAACTCGAGGAGATCGAGGTCACTGAAGAAAGAACGGCGAGAGAAATGGA
 TGTCCAAATCAGCTACCAACCGCCAGCAAGGCGCCTCAAGCACAGAGGCTCCAGTGTGCATCTTTTCA
 GAAGGGCTCGAAGAGAGAGCAAGGTGTGGCTGTGGGAGAGCAAGCGCAAGAAAGAACTCGCAAGCTGC
 TCAAGCGCTCGAAGACAGCAAGCACTGCGAGCATGCGAGCCTCACTGTCTACCCACAGCAACAGCAGCTG
 CAGACGGCGCTTTTGACATCTGGGGCTTTCTGTGCTGACCCAGCGCCACAAATCAAGTACTGGTGCAT
 GAGGACATCAATGAGACTCAATTTCTCTCTGTGTAATTTGCAATCTGGCTCTAGATAGTTTGTATCTCA
 ACAGACCCCTACAGCTCATGTAATGCTAGTGAACACTGGACAGGATGTCTCAACAGCTACAGCTACAG
 CTCTGTGAGCTGAGGAGCTCGAAGGTTTACAGAGCATGTAAACCCCGGACTCGAAACATGGAATCTGGATGGAG
 AAGCTATGACATACAGSCAGTTTCAGGCTCGAAAGTGGCAGAAATGAAGACCTTCTTCCAAATCTAGG
 GACACTGTGGGAGAGCTGGGAAGTGTGTAACAAACACAGAGTGGACTCCAAAGAAATAGAGGACTCACTGA
 CTGACAGGCAATGAAAAACCTGTGGGTGATTTCAGCAGCACTGTGCTATTTGGCAGAGGCTCGAAGAGC
 AAGCAGCACTCTGACATCAATGACAGATTTCTGGAGATAACCAAGCAGGACGAGATGATTACTCAGGAAGTC
 ATTTTGGCCCTGCTTTTGTCTTGGATTATACCTCACAGCTGCACAAATGCATTTTTCGATCAAAAGT
 ACCATAAGCCCTCCCGAGAGCTCAACAAAGGAAAGCGAGAGAGCGAGAGAGATTTCTTGGAAATTT
 TCCCAAGGGCGAAGTCAATGGAATTTTAAATCATAGGGAAGAACAGCTCTGTTTCAAATCTCTATTTCCT
 TTGGTTTGTCAACAAAGAGGAATAGAGAGCAGCAGAGGCAAGCTGGAGAGCTGAAACAGCTGCAGAGAC
 TTTGCAATGAGTCACTGACGACAAAGAGATGACATTATACGACATATAACCTGTGGTCTCTGTGACGAA
 CTGGCTCTATTGTATATATGTGACATTTACATGTAATCAACATGGGAATTTTAGGGGAACCTATAAGAAAT
 CCCAATTTCCAGAGTGGTGGTGCATAAACCGCTCTGGCCAGTGTAAAGAAAGAA

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRNRINRPNILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFIFNAFVTPMCCPSRSSLLTGKYVHNHNTYTNNENCSSPSWQQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWGLLKNSRFYNYTLCRNGVKEKHGS
YSKDYLTDLITNDSVSFFRTSKMKYPHRPLVMVISHAAPHGPEDSAPQYSRLFNPASQHITP
SYNAPNPDKHWHIMRYTPGMKPIHMEFTNMLQRKRLQTLMSVDSMETIYNMLVETGELDNT
YIVYTADHGHIYQGFLVGKSGMPEYFDIRVPYFVRVWENSAEGLCNPHVILNIDLAPTILDI
AGLDIPADMKGKSLIKLLDTERPVNRFHLKKMRVWRDSDFLVERGKLLHKRDNKDVAQEBE
FLPKYQVRKDLQRAEYQTACEQLGQKWQVEDATGKCLKHKCGPMRLGGSRALSNLVPKY
YGGQSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKGGDFSFGTGGLEDYSAANPIKVTHRCYILENDTVQCDDLKYK
LQAWKDHKLHIDHETETLQNKIKNLRVGRHLKKKRPEECCHKTSYHTQHKGRLKHRGSS
HFFRKGLQEKDKVWLREQRKKRKLRLKLQNNDCSMPLGTFQDNQHWQTAPFWTLG
PFCACSANNTYWCMTINETHNLFCEFAFGLEYFLDNTDPYQLMNAVNTLDRDVLNQL
HVOLMELRSCYKOCNPRTRNMDLGGSYEORYOFORRKKWPEMKRPSKSLGOLWEGWG

FIGURE 48

AACAAAGTTCACTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCA**GATG**CTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGCCCAGCCTTGGCCCTTCCGGCGCGGGGCCACCTGGGAATCTTTACAC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGC**TGA**GGCTGCTGTGCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTAATATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTTT
GGTTTGAGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFR
RRHGLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPRHHPRHAR

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FIGURE 50

GCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAAAGTGAGTGCTGGGTCACCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCAACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCCTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAAGCTTGGAAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACTGGGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCTCCTGCAGTGCAAGTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGTTCTGTAGGGACCTGACTTCCCCTGC
 TCCAGGCCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACAGCCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
 ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTTTACCTGGAAAAAA
 AAAAAAAAAA

MSDLLLLGLIGGLTLLLLLLTLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTLISWLATRRVHPALDITYIKERKLCAYPRLEIYQEDQIHMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSVSVLEVSPGSRETSAATLSPGAS
SRGWDGDGTRSEHSYSESGASGSSFELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

CCCGGGGAACGCTGTCTCGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGTCA**ATG**ACCTGCGCCCTCACTCTCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGC GGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGG
CCCTCCAAGTGGAGACCTTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGG
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTA'TATTGACACCTCCCT
GACCAGAGACCTCTGTTATAGAACTTGCCCAAAAGCAGGTGATTCAGGCTCTGGAGCAGA
GTC'TTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGCGCTAT
GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCTCTGGTAG
GGATGGCCATGTGCCAGCCCTCTGGGCTCA'TTGGGTACCACTATACAGAAAGGCCAAT
AGACCCAAGTCTTCCAAAAGAAGCTCAAGGAAGAGAAACCAAGACGCAAAAGAAAT**TA**
ATAATAATAAATTTTAAAAAACTTAAAAA

[illegible]

0609 *Chrysomelidae*: *Chrysomelinae*: *Chrysomelini*. New species from China (Coleoptera) [in Chinese with English summary]. - *Zhongguo Xuebao*, 2007, vol. 48, no. 1, pp. 1-4, 1 fig.

FIGURE 54

CCCGGGAACGTGTTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAGAAATAATA
AATAATAAATTTTAAAAAAGCTTA

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FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAAGTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAATAATAAATTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGCTCGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGTCCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGCTCGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCTAAACAACAACCAAAAATCTATTGTGGTATGCACCTGATTAACCT
 ATAAAATGTTAGAGGAACTTTCATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAATAATAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTGTGCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATTCCTCCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAAGTGGCTTTTGGGGTCTCCAAGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACAGGCTCCCTGTGTCCCTTCCATGGGAAGGCTTCCGCTGTGCCTCTCATT
 CCAAGGCGAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDAAVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKEFGRTEDLWQ

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TTCTTGGCTAAAAATCGGGGGAGTGAGGCGGGGCCGGCGCGGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTA
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTATTTATCCACCATGAAAGAT
TTCACCACCTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCAATTTGGCTTTTCGTTGGTTTACAGATGTTGGCCTTTGGGATCTCTGATTGCATCTATGTGG
ATTCCTTTTGGAGGTTATGTGCTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTTCATCTTTTTGGAGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGCTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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FIGURE 62

GGGAGGCTGTGNCCGTTTTGTGTTTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCGGGAACCATTCACGACGGGTGGACTGACCTGAAAAAATGTTTG
GATTINTAGAGGGCTTGAGATGCTCAGAAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

CGACGCCGGCGTGA**ATG**TGGCTTCCGCTGGTGTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC
TCTCAGAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAGATGTCTC
AAACGCCGCCAGCGCCCTGGTAACGTACAAAGGAGGCCAGGAAGAAGTTCTCAAACAAGC
TTTTCTACGCCAACCAAGTCCCGGAGAAGCTGGATGTGGTGGTAATTTGGCAGTGGCTTTGGGG
GCCGTGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCAGTCTGGTGGTGGAAACAAT
ACCAAGGCGAGGGGGCTGCTGTCTACCTTTGGAAAGAAATGGCCCTTGAATTTGACACAGGAAT
CCATTACATTTGGGCGTATGGAAGAGGGCAGACTTGGCCGTTTTATCTTGGACCACTCACTG
AAGGGCAGCTGGACTGGGCTCCCTCTGCTCTCCTTTTGACATCATGGTACTGGAAGGGGCC
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTACGGGCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAGCTGGTTAAGGTGGTATCCCA
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCATTGGCCGCTGCTTCAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTGTGACGAGCTGGGGGGCTCCTCTGAGCTCCAGGCAGTACTGACTACATCTCCCA
CTTACGGTGTCAACCCCAACCAAGTGGCTTTTCCATGCAGCGCTCTGGTCAACCTACTAC
ATGAAAGGAGGCTTTTATCCCGAGGGGGTCCAGTGAATTTGCCCTCCACACCATCCTGT
GATTACGCGGGCTGGGGGGCTGTCTCCAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTGCTAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC
CCCCATGTGGTCTCAACACAGGACTTCTAACACCTATGAACACCTACTGCCGGGGAAGCG
CCGCTGCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGGCGCCGGCTTAGGCATGACCT
CTGTTTTCATCTGCTGCGAGGCACCAAGGAAGACCTGCATCTGGCTCCACCAACTACTAT
GTTTACTATGACACGGACATGGACAGGCGATGGAGGCTACGTCTCCATGCCAGGGAAGA
GGCTGCGGAACACATCCCTCTTCTTCTTCTCGCTTTCCCATACGCCAAAGATCCGACCTGGG
AGGACCGATTCCAGGCCGCTCCACCATGATCATGCTCATACCACTGGCTTAGGATGGTTT
GAGGAGTGGCAGCGGAGTGAAGGGAAAGCGGGGACGTGACTATGAGACCTTCAAAACTC
CTTTGTGGAAGCCTCTATCTAGTGGTGGTGAACCTGTTCCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTACCAACCACTTCTATCTGGCTGCTCCCCAGGTGGC
TGCTAGCGGGCTGACCATGACCTGGGGCCGCTGCCACCTTGTGTGATGGCTCCTTGAGGG
CCAGAGGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGACTGGTGG
GGGCCCTGCAAGGTGCCCTGTGTGACAGCGGCCATCTTGAAGCGGAATTTGACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCAAGAAAGAAAGAAAT**TAG**TTCATCAGGGAGG
AGTCAGAGAAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGCAGTATAAAGCACTCTAATTTGGTTCTGATGCTGAAGAGAGGGCTAG
TTTTAAATCACAAATCCGAATCTGGGGCAATGGAATCAGTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATGACTTGGATAGCTTGTATG
TCTCATGACGAGCGGGCTCTGCATCCCTCACCATCCCTTAACCTCAGTGATCAACAGCGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGCTAGCTCAACCTGGTGGGTCTAGTTC
TGTCTGAGGCTCTGTCTCTCATTTCAATTTAGTGTCTACGCTGCACAGTTCTACACTGTCAAG
GAAAGGGGAGACTAATGAGGCTTAACCAAAACCTGGGCGTGGTGTGGTTGCCATTCCATA
GGTTTGGAGGCTCTAGATCTCTTTTTGTGCTGGGTTCACTGGCTCTTCAGGGGACAGGAAAT
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGCATGTAGTGCATATCCAAATTCATATGGAAGTCCCGGCTCTACAGTCAAGGATCAGG
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGAGTCACTACCTGAGCCTCAATCAAGC
CTTATCCACCAATACACAGGGAAGGTTGATGCAGGGAAGGTTGATCAGGATCAGGATCAGGGA
TGGACTGGTAAGATGAATACTTTGCTGGGCTGAAGCAGGCTGCAAGGCATTCCAGCCAAAGG
CAGCAGGAGGACAGTGCAGGAGGTGTGGGTTAAGGAGGAGGATCAGATCAGGAAAGGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCAATTTGCACTTAATAGCACATGTGAGG
TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCACTTATGCTTTT
GTATCAGACATACGAAGGTCTCTTTCTAGTTCGTGTTAATGTAACATTAATAATTTATTG
ATTCCATTGCTTTAAAAA

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MWLPVLVLLAVLLAVLCKVYLGLFSGSSPNPFSEDKVRPPAPLVTDEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFMSHALLVNHMYKGGFYPRGSGSEIAFHTIPVIQRA
GGAVLTATVQSVLLDSAGKACGVSVKGHELNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTEDLHLPTSNYYVYDMDQAMERYVSMPREAAEH
IPLFFAFPSAKDPTWEDRFGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLFQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCTGLVGLAQALLCSSAILKRNLYSDLKNLDSRIRAOKKKN

[illegible]

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTTLTSDSESVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPAITAIEGTAHG
EPCHFPFLFLDKYEYDECTSDGREDGRLWCATTYDYKADEKWGFCFTEEEAAKRRQMGEAEMM
YQTGMKILGNSKKSKREAYRYLQKASMNHTKALERVYSALLFEDYLPNQLQAAREMEFEK
LTGEGSKGOTAGFLGYASGLGVNSQASNAHLVYTFGALGGNNIAHMLVLSRL

CTTCCCAGCCCTGTGCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTTGGCCATGGCCTGCCGGTGCCTCAGCTTCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTTGGCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGCTCTGG
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCCTCGGAGGAGGATCA
CCACCGGCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCTACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCACAAC

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTTISPVQPEDDADYYCSVGYGFSF

FIGURE 69

GCGGCCCGCCCCGAGACCGGGCCCGGGGCGCGGGGCGCGGGATGCGGCGCCCCGGGGCGG
 CGATGACCGCGGAGCGGACCGCGCGCGGCCCGCCCTGACCCCGCGCGCGCCCGCGTGAGCCCC
 CCCCCGAGGTCGCGACAGGCCGAGATGACCGCGAGCCCCCTGTGCTGCTCTGCTGCCGC
 CGCTGCTGCTGGGGGCTTCCACCGGGCGCGCGCGCGCGGAGGCCCGCCCAAGATGGCGGAC
 AAGGTGGCTCCACGCGAGGTGGCCCGGCTGGGCGCACTGTGCGGCTCAGTGGCCAGTGGG
 GGGGACCCGCCCGCTGACCATGTGGACCAAGGATGGCGACCATCCACAGCGCGCTGGA
 GCGGCTTCGCGGCTGCTGCCGAGGGGCTGAAGGTGAAGCAGGTGAGCGGGAGGATGCGGGC
 GTGTACGTGTGCAGGGCCACCAACGGCTTCGGCGAGCTGAGCGTCACTACACCTCGTCTGT
 GCTGGATGACATTAGCCAGGGAGGAGAGCCTGGGCGCCGACAGCTCTCTGGGGGTCAAG
 AGGACCCCGCCAGCAGCATGTGGGACAGCCGCGCTTACACAGCCCCFCCAAGATGAGGCGC
 CGGGTGATGCGACGGCCCGTGGGTAGCTCCGTGGGCTCAAGTGGTGGCGAGCGGGCACCC
 TCGGCGCGACATCAGTGGATGAAGGACGACAGGCGCTTGACGCGCCAGAGGCGCGTGAGC
 ACCTGCGGTAAGAGTGGACTGAGCCTGAAGAACCTGCGGCGGAGGACAGCGCAAAATAC
 ACGTCCCGCTGTGCAACCGCGGGCGCCATCAAGGCCACTACAAGTGGATGTGATCCA
 GCGGACCCGTTCCAAGCGCGTGTCTCACAGGACAGCCCGTGAACACGACGCTGGACTTCG
 GGGGACCCAGCTCTCCAGTGAAGGTGGCGAGCGACGTGAAGCCGCTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCGGAGGCGCCCAACTCCACATCGATGTGGCGGCCAGAA
 GTTTGTGGTGTGCCACGGGTGACGTGTGGTGGCGGCGCGGAGCGCTCTCACTCAATAAGC
 TGCTCATCACCCGTGGCGCGCAGGACGATGCGGGCATGTACATCTGCTTGGCGCCAAACCC
 ATGGGCTACAGTTTCCGCGAGCGCTTCTTCCACCGTGTGCGAGCGCCAAAACCGCGAGGCC
 ACCTTGGCGCTCTCTGCTTCTCGGCCACTAGCCTGGCTGGCGCTGGTCTCATCGGATCCGAC
 CGGGCGCTGTCTTATCTTGGCACCTGCTCTGTGGCTTTGCCAGGCGCCAGAAGAAGCCG
 TGCACCCGCGGCTGCCCTTCCCTGCTGGCACCGCCCGCGGGGAGCGCGCGGACCG
 CAGCGGAGACAAGGACCTTCCCTCGTTGGCGCGCTTACGCGCTGGCCCTGGTGTGGGGCTGT
 GTGAGGAGCATGGGTCTCCGCGAGCCCCCAGCACTTACTGGGCGAGGCCAGTGTGCTGGC
 CCTAAGTTGATCCCCAACTTACACAGACATCCACACACACACACACACACTCTCACAC
 ACACCTGCAGCTGGAGGCAAGGTCCACCAGACATCCACTTACGTGCTAGACGGCAGCGCT
 ATCTGCAGTGGGCGAGGGGGGGCGGCCAGACAGGACAGCTGGGAGGATGGAGAGCGAGCT
 GCAGACGAAGCGAGGGAGCCCATGGCGAGGGAATGGCGAGCACTCCAGGCGAGTGTGTGT
 TGAGAGCATAGCCCTGGACACACACACAGACACACACACTACCTGGATGATATGTATGCAC
 ACACATGGCGCACACAGTGTCTTGAAGGCACACGTACGCACACACATGCACAGATATG
 CGCGCTGGGCGACACAGATAAGCTGCCAAATGCACGCACACGCACAGACATGCCAGAACA
 TACAAGGACATGCTGCTTGAACATACACACGACACCCCATGCGCAGATGTGCTGCTGGACA
 CACACACACACAGGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACACA
 CAGTGCACAGATATGCTGCTGGACACACAGATATGCTGCTTGCATACACACATGCACGG
 ATATTGCTGGACACACACACACACACGCTGACAGATATGCTGTGGACACGCACAC
 ACATGCAGATATGCTGCTGGACACACACTTCCAGACACAGTGCACAGGCGAGATATGCT
 GCCTGGACACACGAGATATGCTGTCTAGTCAACACACACGACAGATGCTGTCCGGACAC
 ACACACGATGCACAGATATGCTTCCGGACACACACACGACAGATATGCTGCTGGAC
 ACACACACAGATATGCTGCTTCAACACTCACACAGTGCAGATATGCTTGGACACACACA
 TGTGCACAGATATGCTGCTGGACATGCACACACGTCAGATATGCTGTCCGGATACACAGC
 CAGCACACATGAGATATGCTGCTGGGACACACTTCCGGACACACATGCACACAGGT
 GCAGATATGCTGCTGGACACACACAGATATGCTGCTTCAACACTCACACAGTGCAGATA
 TATTGCTTGGACACACACATGTCACAGATATGCTGTGACATGCACACAGTGCAGATA
 TGCTGTCCGATACACACGACACACATGCAGATATGCTGCTGGGACACACTTCCGGA
 CACACATGCACACAGGTCAGATATGCTGCTGGACACACGAGACTGACGTGCTTTTGG
 GAGGTTGTGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
 CCGTCTCCACTGCTTCTCCCTGGCTTGGCGGCTATTTTGGCACTGCTTGGTGGCGCCAG
 AGTCCCTTACTGCTGTGGGCTGGGGTGGGGGCGACGAGCCCCAAGCCTGAGAGGCTGGAG
 CCGATGGCTAGTGGCTCATCCCCAGTGCACTTCCCCGTGACACAGAGAAGGGGCTTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATATGATGGAAGGAGACTGGGTGTGAGGAC
 TGTGGTCTCTCTTGGGGCGGGGACCCGCTGGTCTTTACGACATGCTGATGACCAACCC
 GTCCAGGCGACACACACCCCGCCCGCCACTGTGCTGGTGGCGCCAGATCTCTGTAATTTTA
 TGTAGAGTTTGAAGTGAAGCCCGTATATTTAATTTATTTTGTAAACACAAA

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MTFSP LLLLLL PLLLLGAF PAAAAAGP PKMADKVVPRQVAVLGR TVRLQCPVEGD PPLTMT
WTKDGR TIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFSGLSVNYTLVLVDDISPGK
ESLGPDSSSSGGQEDPASQQWARFRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVVDVIQRTSRKFPVL
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFPVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPFAVVIGIPAGAVFILGTL LLWLCAQKKPCTPAPAPPLPGHRRPPTARDRSGDKDLPS
LAALSAGVGVLCEEHGSFAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHSHSHEGVK
HOHIHYOC

FIGURE 71

CCGAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTCTCCCAGGGGACCCGATTCACAGATC
 AGTGAATCTGTGAGACACCCATCTACCTCTTGCCACGTTCCACCGGGCTTGGGGGAAAGATGCTGGGGACCA
 AGGCCTGGGTGTTCTCCTCTCTGGTCTGGAAGTCACATCTGTGTTGGGGAGACAGACATGCTCACCAGTCA
 GTAAGAAAGAGTCCAGCCTGGGAAGAAGAACCCAGCATCTTTGCCAAGCCTTGCCGACACCCTGGAGAGCCCTGG
 TGAGTGGACACATCTGGTCAACATCGATACCCAGGGAGGGAGGAGCTATGAGCGCTGGAGCCTTTGGT
 TCTACTATGGGAGCCTGTATCTGCCCTGCTCCGCGTAGAGGCTGGACCTGACTGGACATCGAGCCGCTGG
 AGCACTGGCCAGGTGGTCCATGGTAGTCCCCGTGAGGGTTTCTGCTGCCCTCAACAGGGAGCAGCGGCTGGCCA
 GAAGCTGCTCTAATTACACGCTACGCTCTCTCTGCCACCAGGATCCCTCGCCGAGACACAGAGCGCATCTGGA
 GCCATGGTCTCCCTGGGCAAGTGCTCAGCTGCCCTGTGGTCAGACTGGGGTCCAGACTCGCACACCGCATTTGCT
 TTGGCAGAGATGGTGTGCTGTGAGTGAAGGCCAGCGAAGAGGCTCAGCATGAGTGGCCAGGAGCTGTACAGC
 CTGTGACCTGACCTGCCCATGGCCAGGTGCAATGCTGACTGTGATCGCTGTGCTGCCAGGACTTCAATTTCT
 ATGGGCTCTCTCCTTCCGAGGTGCCCAGCTGCGAGGCTGTATCTAGCTGCTGCTACACAGAGCCGGAAG
 CTGCTGACCCAGACAGACAGTGAATGGGAGATTCCGAATCCCTGGCTTTGTGCCCTGATGGCAAGACATCTGAA
 GACTCACAAGGTCAAGTTTGGCCCCATTGTACTCAAAATGCCAAGACTAGCCTGAAGCCAGCCACCATCAAGG
 CAGATTTTGTGAGGGCAGAGACTCCATACATGGTGATGAACCTTGAGACCCAGGAGAGCTGGGCGAGCG
 GTGTCTCTGCTCTGTAAGGCCACAGGGGAAGCCAGGCCAGACAGTATTTTGGTATCTAATGACACATTTGCT
 GGAATCTTCTCTTACAGCATGAGGAGAGCTGTGTGAGGAACTGAGCAGACCCGAGAGCTGGGAGTGAAT
 TTGCAAGGCCAGAGTGTGCPGGGCTGTGAATCCAAAGTTGCCAGCTGATTGTCAAGCATCTGTATGAG
 ACTCCTTGCAACCCAGTTCTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCAGAATGCCACCACCTC
 CTCTACTATGACGTGGGACGCTGCCCTGTTAAGACTTGTGAGGGCAGCAGGATAATGGGATCAGGTGGCGGT
 ATGCTGTGACAGACTGCTGTGGCATCTCCAAAGACAGGAAAGGGAGATCCAGTGTGAGTGGCTACACGCTTACCC
 ACCAGGTGGCCCAAGGAGTGCAGCTGCCAGCGGTGTACGAAACTCGGASCATCTGTCGGGGCGCTGTCTAGTG
 TCTGTGAATATGGGAGCCGATCGCTTGTGCCATCTGTACATGGGAAACGCTGTATAGCATGACTGGCTACA
 AGGCACTTTCACCTCCATGTCTCCCAAGGACACTGAGAGGCTGGTGTCTACATTTGTGGACAGGCTGCAGAG
 TTGTCAACACCACCAAGTGTCCCTTTCAACAAGAGGGGGAGTGGCGTGTCCATGAATCAAGTGTACCTTCC
 TCGGAAGAGGACCATCACTTTGGAAGCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGGTGTGGTGAAGACC
 CCATGGCTGACCATGGAGATTTCATCCAGGAGTTTTCACAGGCAAGATGGGGAGCCCTACATGAGAAAGTGAAG
 GCCAGTGTGACCTCTCTGGATCCCGGAATATTTCCACAGCCAGCAGCTGCCAGCATCTCAATGAACATTCATCA
 TGAACGAAGAGACATTTCCCTCTCGGCGATTTCTGTGGAATTCAGAGTGAAGTCACTGAG
 AGCCACTTAATGCTGGCCAAGTGAAGGTCCACCTTCACTCGACCCAGGTCAAGATGCCAGAGCACATATCCACA
 GTGAAACTCTGTTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAAGTGTATTCAAAATTTGAATCAAG
 GAGGAACAAAGAGAAGACAGAACCTTCTGTGGGCAACCTGGAGATTCTGTGAGAGGAGGCTCTTTAACTGG
 ATGTTCTCTGAAAGCAGCGGCTGCTTTGTTAAGGTGAGGGCTACCGGATGAGAGTTTCTTGCCTAGTGAAGCAG
 ATCCAGGGGTTTGATCTCTGATTAATCTGTGAGCTAGAACTGGCTTTCTTCAACCTAGGCGCTGGGG
 CGGCTTTGACGTGTCATCAGAGCCCCAACGGGCTGTGTGCTTCTGTGATGACCAATGCCCTGTATG
 CCTACTCTGCTTATGTTCTTGGCAAGCCTGGCTGGGAGGAATCGAAGCAGTGGAGTCTTCTCCTAATATCAAC
 CCAAGATGCAATTTGGCTTCCCTCAGCCCTATCTCAACAAGCTCAACTACCGTCAGCAGGACATGAGGATCCAG
 GGTTAAAAAGACAGCTTTCCAGATTAGCATGGCCAGGCCAAGGCCCACTCAGCTGAGGAGAGCAATGGGCCCA
 TGTATGCTCTTGAGAACTCCGGGATGTGAAGGACACACCCAGCTGAGCCCACTTCCGGTTCTTACAGATTT
 GAGGGGATGATGATGACCAACACGCTCCCTTCAAGAGATGACCATGAGTGGCTGATGACATATCT
 GGCATGTGGCCACAGGACCGATGAATTCAGGGCTGCTATATCAAGGTGAAGATTGTGGGGCCCTGGAATGTAT
 ATGTGCGATCCCGCAACATGGGGGCACTCATCGCGGACATCGGGGAAGCTGTATGGAATCCAGATGTGAGG
 AGCACTCGGGGACAGGGGACAGCCCAATGCTCAGCTGCCCTGTGGAGTTCAGGTGAGTGGGATGCTCTATGTA
 TCAGGAGGCTGTGGACCGCACCTCTGTTGAAGTCACTCCCGAGGCGAGCTCGCTCGAGCCAGTGTGAACCCCA
 TCTGCACTGAGTACTGCTCAACATCTGGCATTTCTAGTCAACACAGCAGCAGCAGTACGATGACCATGTGGG
 CCTTTGGACCTGGGCGCACTATGGCATTTGACCTCTCACTGACAGGACGCTGCGACGGCCAGAGAGAT
 CGCGCTCGGCGGTTGCTTTGATGGCACATCCGATGGCTCTCCAGAATCATGAAGAGCAATGTGGGAGTATGCC
 TCACCTTCAACTGTGTAGAGAGGCAAGTAGGCCGCGAGATGCCCTTCCAGTACTCCAAAGACCCCCAGCCAG
 TCCCTGCTCGAGGACCTGTCCAAGGAAGATGCCCTCGAGGAGGACAGCAGGAGCGAGGGGTGGCCAGCG
 CCAGGCTGGAGTGGTGGCTCTCTGAGATTCTCTAGATTGCTCAACAGCCCTTGATCAACTAACTTTTGTGGT
 ACTTCACTCTCTCTGCTCTCATTTCTGTGACACCCCTGTGTGAGTGTGATGATGCAAACTGTGCTGGTAT
 TTAAGCACTTTGTTCTGTGAATTTGCTTTGTTCTTCTATGCTCTTACTTGTGCTCCATGCTACGACA
 TTGGCACTGGGCCCCACAAATGGCAATAAAGCCCTTTTGTGAAACTGTTTCTTAAATGAACACAGAAATAT
 GGCCATCTGATAAATCTCGACTTCAACTGTACTTCAATTTGATGCCAATATGATCAAAATATACTCTCTTCTT
 TTTGCAATGGTTTGGCCCACTCTGCAATAGTGATAATCTGATGCTGAAGTCAAAATAAACATATAAGCATAT
 TTTTGGCTCTCTCAAGGACATGGCAGGCTTGATCATGTTCAATCAATAAATGGTGGTGAATTAAG
 AATTAACACATATCTTCTCTGATTAATTAATTAATTAATTTCTTGTGATTAATTAATTAATTAAG
 ACATTCAAAGTTAAGCTATTAATATAGGTGATCATAGTTCTCTCAACAAGTCTGAAAGAGCTCTCTGCT
 ATCCAAATTACACAGGTTGCTAACTGTATTGTACAAATTTCCCTTGGATTCGTTTGTGTTGCTAGAAAC
 CCAGTGTAGCCGGGAGATGCAATAAATGCATCTGTATTTCGAAAAA

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPISIFAKPADTLESPGEWTTWFNI
DYPGGKGDYERLDAIRFYYGDRVCARPLRLLEARTTDWTFAGSTQGVVHGSPREGFWCLNREQ
RPGQNCSNYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLT
TPKLLTQTDS DGRFRI PGLCPDGKSLIKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKVLRLKQQHAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPVPE SYLIRLPHDCFQ NATNSFY YDVGRCPV
KTACAGQDNGIRCRDVAQNCGSGITKEERTICSGYTLPTKVAKESQCRCTETSVIRGVR
KADNGEPMRHFHVMYDGNVRSMSTGYTEFTLTHVPDLTFVDRLQKFVNTEKVLFPFN
KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGDEPMAELEIPRSRFRQNGEPIYIGKV
KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
DVPESRRCFVKV RAYR SERFLPSEQIGGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNYYRTDHEPR
VKKTAFAQISM A KPRPN SAEESNGPIYAFENLRACEEAPSPA HFRFQIEGDRYDYNTVPFN
EDDPMSWTE DYLA WWP KMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSRRASVNPMLHEYLVNHLPLAV
NNDTSEYTM LAPLDPLGHNYGIYITVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
FNCVERQVGRQSAFAQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA
OOPLIN

FIGURE 73

CTGCAAGTTGTTAACGCCATAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCCGTACGCATACATACATATGTGTATATATGTAACCTAGACAAAAGATCCGAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTAGAGATGTTATTTGTCAGAGTCCCTGTCGATTCATG
 CCTTTTGGGTTACGGTTTCCAGTGTGATGCAGCCCTACCCCTTTGGTTGGGGACATATGATTTTGTAGAGCT
 CAGATTACACGGAAGAAGGGAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCAGGCATGACAAAAATA
 TCTGAAAGTGAACCTGCATCTCCCGATATTACCTGTGGAGACCCCTCTGAGACGTTCTGTGCAATTGGGCAATC
 CCTACATGTGCAATTAATGAGTGTGATGCGACTACCCCTGAGCTGGGCACACCCCCCTGAGCTGATGTTTGATT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGAAAGGATATCCCAACCTCTCCAGGTTAATCAT
 CACTCTGTCTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTTATCAGACGATACGGTCTTAGAAATCATTTGACACAGA
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTGCGCTTTTGTG
 CTGGACCTCGCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAATCAGAGATTTCTTT
 ACAGT CACAGCCTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAAATCTCCATGCCACTGTATGTG
 TGTATGACAAACGAAATTGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATCGAAGAAG
 AATATATCAGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCCTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACACAGAGCTCCTGCCTGCCAGAACGGAGGACGTGCCACA
 ACAACGTGCGCTGCTCTGCCCGGCCCATACACGGGCATCCTCTGCGAAGAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCGCGACGGCACCCGACGCTGTGCTGTGACCCAGCTGCT
 GGGAACCGCCAGCCCTCGTGTCTTACAGTGTCACTCCAGCCACACCGGACGGGCTGTGCCGTGGGGAAGCA
 GACACACCCCAACATTTGCTACTAACATAGGAAACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAGAAGGCCATACTGAATTAAGCCATATTTATCACCCGTGGACAGCATCCGAGTCAAGACTGTTAATTTCT
 TGAATCCAGGAGGATTGGCAGCTGTTGATATTACCTGCAAAATCACATTGCCAGCTGCGAGAGCATATTGTGGA
 TTGGAAGGCTGCGACAGCCCCCAACAGGAAGACAAAAACAACAAATCAACCGACTTAAAAACATTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTTGTGGACCAACCAATAGCATCTTTGCTGTAG
 GTGCATTGTGGGCATAAGGAATCTGTTACAAGCTGCCATATTGGCTGCTTCCGTCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTGGTTGAAAGATTTCTTGTCTGTATGTAGTGATGCACA
 TGTGTAAACAGCCCTCTAAAAGGCGAAGCCAGTCAATCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGGA
 GCACACACCCCATATACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCTCTTTGTATTCAATGAAGTT
 ATTTTCTTGAATCTGTTAATATGTAGATTTTGTATTATTGGCAATTTGTGTTTACGACAAATCTGTTAAT
 GTATCTATTTCCGATCAGCAAGACTGACATTTTATTTTGTCCTCTTTCGTTCTGTTTGTCTACTGTGCA
 GATTTCTCTTAGGGCAACGACCTGCTGGCATCAAAGATATCAGTTACATATAACAGTGTAAATAAGA
 TTCCACCAAGGACATCTTAATGTTTCTTGTGCTTTAACACTGGAAGATTTAAAGAAATAAAATCTCTGCA
 TAAACGATTTTCAAGATTTGTATTGCAATTTCTTAAGATGAAGGAACAGCCCAAGCAGTTTCACTCACT
 TTAAGTATTTCTGTGGAGTGAATACATTCACTGACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACACAGCAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRWQPYQYYATDCLDFAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFFTVTDLRIRLLRPVAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCKGCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTLLGTAS
PLVF

0000727.11901

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCGGCTAAGATTGCTGAGGAGCGG
 CGGGTAGCTGGCAGGCGCCGACTCCGAAGGCCGCGCTCCGGGCGAGGTGTCTCATGACTT
 CTCCTTGTGGACATGTCCGTGATCTTTTTTGCTGCGTGGTACGGGTAAAGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCGACTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTCGGAGACCTGTGGTGGGAATTCACAGCTTCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTGAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACTTGAGGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTGAGGAGTTCACTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACTCTGTGAGCCAGCCACCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAATCTTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGCGATGTGAGTGAATCTGGGAATGGCTGGATTTCGGAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGT
 GCTTTCAGAAGTGTTATTTTCATGAATCATTATATGATTTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTTC
 TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAAACTTGATAAAAAGTGTGTAATAATGTATAGCCATTTATATCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTAATAAAAAAAAAAAAAAAAAA
 AAAAG

MSVIFFAFCVVRVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLRGVHLAEHSLQDPRSWFCWLDQTS

TGCCTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAGAAAAGTGAAGTGGCATT
 TTAACATATGAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAATGGGGT

CTCAGCGCGCGCTTCCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCA
CCCCGACCTTAAAGAGTGGGAGCAAAAGGAGGACAGAGCCCTTTAAACAGAGCGGGTGGTG
CCTGCCCTTTAAAGGCGGGCGCTCCGGACACTGTATTCTGAGCCCCAGACTGCCCCAGATT
TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGCGGCTT
CCTCCCGGCTGCTCTCCCGGGCCAGAGGACCTCGGCTTCAGTCACTGTCAGCAGAT**A**
TGGAGCAACCTGACTAGCAAGTGCATTCGCTGGCAGAAACAGTATTCCAGAGAGGATCCG
GAGTGATTATATCAACACTTCTGTTTGCACACTGTACATCTCTCGCCACATCTTCCCTGA
CCGCTTCAAGAAAGCCTGCTGAGTTTACCACAGCTGGATGATGAAGTGCACACCTCAACAAG
TTGCGCTGAGGCTGTGCACTTTACCTTGCAATTGCCCTGGGTGCTGTCTGCTCTCGCC
TTCTCCATCATACGAATAGGTGCTGCTCTCCCTGCCCTCGGAACCTACATACATCAGTGGCT
CAACGGCTCCCTCATCCATGCCCTCTGGAACCTTGTTTTCTCTCCCAACAGTCTCCCTCA
TCTTCTCATGCCCTTTGCATATTTCTTCTACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCTCTCACTGCTGGTGGCT
AGGATGGTGTGGGTGGCATGACCAATTGTGGAACAAGAACAGGCCAACAGAGTCACTCT
ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCTATCTCTCTCTTGGGGTCTGT
CTGCTCTGGTGTGTAATCCACTGGGTCTTGGCCGCACTGTTCTCCGTCACCTGGGAAGTCT
AGTCAAGCGCCGCTGCTGGAAGACTGGAGGACAGGCTGTAAGTCTCAGCCTTTAGAGGCT
CAGCCGCTGACCCGAGGATCTGTAATCTCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTG
TACACAGACAGGCTCTGGCTCTGCAGACACAGAGGCTCTGCTGGAGAAGAGGCCGAAGGCT
TTCAGCCTGGCAACGGAACCTGGGCTTACCCCTTGGCTATGCTGTGCTTGTGGTGTGCTGACGG
GCCGTGCTGTGCTCATTTGTGCCATCCATATCTCTGGAGCTGCTCATGATGAGGCTGCCATG
CCCGAGGACTGACGGTACTCTTATGGCCAGTGTCTCTCTTCCAACTGGGCTCCTTTGG
TGCCGTCACTTCAAGTGTGTAATCATCTTTTACCTAATGGTGTCTCAGTGTGGGCTTCTATA
GCTCTTCACTCTTCCGAGGACTCGGGCCAGATGGCAGCAGCTGACCGAGATAATT
GGGAATCTGTGCTGTCTTCTGTGCTTAAGCTCAGCACTTCTGTCTTCTCTGCAACCTGGG
GCTCACTCGCTTTGACCTGCTGGGTGACTTGTGGACGCTTCAACTGGCTGGGCAATTTTACA
TTGTGTTCTCTACAACGACGAGTCTTGCAGGCTTACCACACTGTCTGTGGTGAAGCACTT
ACTGAGCTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGTGCCGCT
CTCCGGTTTCCCCAGGCATCTAGGAAGAACCCAGACCA**GTG**ACTCCAGCTGGGGTGGGA
AGGAAAAA**CT**GGACACTGCCATCTGCTGCTTACGGCTGGAGGGAAGCCCAAGGCTACTTTGG
ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGGCCATCTGCATTA
TCATAATCTGAGGCAGAGTTTGGGACAGGACCTCTCTGCTTACCACTTAAGTGTGGCT
CAGCATGGGTAAGGCTGGGTGACTGGGTCTAGCCCTGATCCCAAATCTGTTTACATATCA
ATCTGCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGTATGTGCAAT
AGGGTGGGTAGGGCCAGGGAAGGACTGGCCAGGCGAGGCTCGGAGAGTATGATGTCTTCT
CTGGCTCTGGCCCGACAGAGCTTAAGCACTGTGCTATCTCTGGAGGGGCTTTGGACCACTG
AAAGACAAGGGGATAGGGAGGAGGAGGCTTACGCCATCAGCAATAAAGTTGATCCCGAGA
AAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDATVNK
IALELCTFTLAIALGAVLLLFFSIIISNEVLLSLPRNYIYIQLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLGRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYLYPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLEEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLSFGAVIQVVLIFYLMVSSVVGFY
SSPLFRSLRPRWHDAMTQIIIGNCVLLVLSSALPVFSRTLGLTRFDLLGDGFRFNWLGNFY
IVFLYNAAFAGLTTLCLVKTFATAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCCTCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGCGCGGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAAGTGGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTTCCAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

The figure consists of 12 small diagrams arranged in two rows of six. The top row shows the initial impact of a water droplet on a surface, with labels 'a' through 'f'. The bottom row shows the crown's development and the final splash, with labels 'g' through 'l'. The diagrams illustrate the sequence of events from the first contact to the final splash.

CAGAGAAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGTGAGGCGGCCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGGAGGAGGCTGTGAGGAGTGTGTGAACAGGACCCGGGACAGAGGAACCATGGCTCCGAGAACCTGAGCACCTTTGCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTGGGGTGCCTCGAAGTGCTCTATAAAGGATATTTAAAGGCCTATAGGAACTAGCCCTGCAGCTTCATCCCGACCGGAACCTTGATGATCACAAGCCCCAGGAGAAATTCAGGATCTGGGTGCTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAAAGATTAAAGATGGTCATCAGAGCTCCCATTGGAGACATTTTTTCACACTTCTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATTTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGGAAGTAGTGTAGAAACAACCTGTGGCAAGGCAGGCTCTGGCAAACGGAAGTGCAATTGTCCGACAGGATGCGGACACCCAGCTGGGCCCTGGGCGCTTCCAATGACCCAGGAGGTGGTCTCCGACGCAATGCCCTAAGTAGTGAATGAATGAAGAACGCTGGAAAGTAGAATAGAGCCTGGGGGTGAGAGACGGCATGAGTAGCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGGAGATTTACGGTTCGGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATTGTACACAATGTGACAAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACTCACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCTATGGAAGAAAGGGGAAGGGCTCCCAACTTTGACAACAACATATCAAGGGCTCTTTGATAATCACITTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAAACAGCTACTGAAACAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTGATAAAATTTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTTTTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGATCATCATGAAATGAATAAGAGGGCTTAAGAAATTTGTCCATTTGCATTTCGAAAAGAAATGACAGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCTGAGTTTCAAGAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGAGTTGTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTGTTATTTTAA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
 AQEKFQDLGAAYEVLSDSEKRKQYDTYGEEGLKDGHQSSHGDI FSHFFGDFGMFGGT PRQQ
 DRNIPRGSDIIVDLEVTL EEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
 MTQEVVVCDECPNVKLVNEERTLEVEIEPGVRDGM EYPFFIGEGEPHVDGEPGDLRFRIKVVKH
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCCTNGAAGTGCCCTNTATAAAGGATATTA AAAAGG
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGAGGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTGCTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGACGCC
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCGGCCCGCAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTGAAGATTGTGACACTCTGAC
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGCCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAC
 TCACCTGGTGCTGGTGACAAGGAATGCCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGGTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCTCCAGGCCCTGAAGGCTTCTGACGAGCAGTCTGCAATTT**TAG**TGCCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCTGGATGGCTCAGCTTAGCCCTT
 CTACTTTTTCCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTGAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAAC
 ACAAGTTGATGATTTCTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACCTATGTTTCCCTCAAAAAAAAAAAAAA

METVIVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSESEL
 ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLLEKLVAMTMGSGAKMKTSAS
 VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
 DQSLSAEEHLEVLREAAALASEPDKLGPPEGFLQEQSAI

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCCTGGGCTTCCGAGGTGCTTTCGCCGCTGTCC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTCTGTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGAATTGGTTAGAAAGAACATTTCAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAAGTTGGAGAAAGCAACAATATGGTATAACAACA
AGTGAATTTGAAGACTCATTAAAAATATTGTGTTATTTATAAAGTCATTGAAGAATATTCA
GCACAAAATTAATTACATGAAATAGCTTGAATGTTCTTTACAGGAGTTTAAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTTGAAGGCTATTTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCTGTTTCTTTCTTTTATTTGAAGGCTCAGGAGCATCCATAGGCATTGTCT
TTTTAGAAGTGCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDQTQKIGMGLTGFGVFLLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFETIYGFFLLFRGFFPVVVGFIIRRVPLGSLNLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAAATGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

GGCCACGAGGCTGAACCCAGCGCGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAAG
GGCTGCCAGGAAGGAGACGCCTTCTCTGAGTCTGGATCTTTCTCTCTCTGGAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCCTTATTGCCTCAGGGCTAATC
ATCAACACCATTTCAGTCTTCACTCTCCTCTCTGGCCCATTAACAAGCAGCTCTTCGGGA
GATCAACTGCAGACTGTCTATTGCATCTCAAGGCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCAGGAATGCACCATCTTCAGGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
GCCATCTGGTCTCTCAACCACAAGTTTGAATTGACTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCGAGAAGTATTTTTCCT
GATTCAGTGTGAGGGCAGCGGTTTCAGCGAGAAGAAGCATGAGATCAGCATGCAGTGGCC
GGGCCAAGGGGCTGCCTCGCTCAAGCATACCTTGTGCCAGAACCAAGGGCTTCGCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTCAGAAA
TAATGAAATCCAACTGCTGGGAGTCTTAAACGGAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCCTGGAAGACATCCCTGAAGACGATGACGAGTGTCTGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGA
GACGCCCATGGTGCCCCCGCGCGCCCTGGACCTCGTGAAGTGGCTGTTTGGGCCTCGC
TGCTGCTCTACCCTTTCTTCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCTGACG
CTGGCCAGCTTCATCCTCGTCTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTACGA
CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTGTAACTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGAACCTTGTCTGTGATCATAGAAGGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGACGGAAGGGACAGTATCCCCCTTCACTCTTTGGTGTGAGTTTCTGT
AACCCTTGGTTGCCAGAGATTAAGTGAAGAGTGCTTTAGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAAATTAAGTGGCTTTTCTGGGTCAAAAAAAA

MDLAGLLKSQFLCHLVFCYVFIAASGLIINTIQLFTELLLPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRLAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLGGSKVLAKK
ELAYVPIIGWMWYFTEMFCSRKEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPLRLKHLLPRTKGFAITVRSRLNVVSAYVDCITLNFNRNNENPTLLGVNLGKK
YHADLYVRRIPLEDIPEDDDECSAWLHLKYQEKDAFQEYYRTGTFFETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVGRMMIGVTEIDKGSAYGNSDS
KQKLNLD

FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA
 GTAAAGGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTGTGTTA
 TACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTCTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGACAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAAAC
 TGTATCAGGTTCCGTGATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAAGTGGAAGACAGTGAAACAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAACACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAACATCCAAAAAGACCCCTCAGGAGAACATTTTTCTTTGTCAGGCATTA
 CGGACCTTTTTTCAAATTCGAATTTCTTCATTCATGTGTTATGTCTTTAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACACCAACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTACAGGCTCTCTTACA
 TTT**TGA**TCCCTTTTAAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAAGTAAAGTTCATTGTTTTTACTATGTTTAC
 CTGTTTGCAAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCAAACCTTTTTTTTACCTTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAATGGAAGAAGCAAGTATAGCCTTAT
 TTTCAAAATATGGAAGAAATTTATATGAAAAATTTATCTGAGTCATTAAAAATCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGTGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAATTTTTTTTTTTTTTTTTTTTTT

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLEGEVKEAKNSITDSQMDDVEVVYITIDQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIIITESCSTHRLHSLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDDRWFKRSRLLDTDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

FIGURE 96

GGCACAGCCGCGCGCGGAGGCGAGAGTCAGCCGAGCCGAGTCCAGCCGGAGCAGCGGACCAGCGCAGGGCGAGC
 CCAAGCAGCGCGCAGCGCAACGCCGCCGCCGCCACACCCCTCTGCGGTCCCGCGCGCGCTGCCACCCCTCCCT
 CCTTCCCGGCTCCCGGCTCCGCCGCCAGTCAAGTTTGCGGGTTGCTGCCCGCGGAACCCCGAGGTCACCA
 GGGCGCGCTCTGCTCCCTGGGCGCGCGCGCCCTCCACGCCCTCCTTCTCCCTGGCCGCGCGCTGGCACC
 GGGGACCGTTGCTTGACGCGAGGCCAGCTCTACTTTCCGCCCGGCTCTCCTCCGCTGCTCGCTCTTCCAC
 CAACTCCAACTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCTCCGCCCGCTGCCGCTAG
 CGCGCTTCCGCTCCGCTCCCAAGGTGGGAACGCGTCCGCCCGCGCGCTGCTGGCTGCCGAGCTCAAGTCAAAAGTTGCTCGG
 CGCGCTTCTCTGCACCCCTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCAAAAGTTGCTCGG
 AAGTGCAGCGCTTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCGCCCTCCACGAGATCAACCGTGATCAT
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTCCAAAGTAAAGA
 TGATTTCAAAGTGTGTGAGCAACAGTGCATCATTTGCAAGCTGTCTTTGCTTCAAGTTACAAGAGTTTG
 ATGAATTCTTCAAAGAACTACTTGAATAATGCAGAGAAATCCCTGAATGATATGTTTGAAGACATATGCCAT
 TTATACATGCATAATCTGAGCTATTTAAAGATCTCTCGTAGAGTTGAAAGCTTACTACGTGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAATCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTCGGAGATGTCCCT
 CGCAAAATTGAAGTCCAGGTTACTCGTGCTTTGTAGCAGCCGCTACTTTGCTCAAGGCTTACGCGTTGCGGG
 AGATGTGCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCGAGTGTACCATGCCCTGTTGAAGATGATCTACT
 GCTCCACTGCGCGGGTCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAACCATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTTCATAGATGCTATGCTGATGTTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTTGAATCGGTATGGATCCCATCGATGGAAGATTCTGATGCTATTTATGAACATGCAGG
 ATAATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTT
 TCTCGTTCATCTCTGAAGTGCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACACAGC
 AGCTGGCAGTATTTTGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGCTCCT
 CCTTCCGAGCAAGCTTTGCAACGATGAGAGGATGGCTCAGGAAACGGCAATGAGGATGACTGTTGGAATGGG
 AAAGGCCAAAGCAGGTACCTGTTTGCAGTGACAGGAAATGGATTAGCCAAACAGGGCAACAACCCAGAGGTCCA
 GGTGACACCAAGCAACAGACATACTGATCCTTCGTCAATCATGGCTCTTCAGATGATGACCAAGCAAGATGA
 AGAATGCATCAATGGGAACACAGTGGACTTCTTGATATCAGTGATGAAAGTAGTGGAAGAGGAAGTGGAAAT
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGAACATGCTGGGAAGAGTGCCAAATGA
 GAAAGCCGACACTGCTGGTCCGCTCTGGGCGACAGGCCCTACCTCCTCACTGTCTTCTGCATCTTGTCTCTGG
 TTATGCGAGAGCAGTGGAGATTAATCTTCAACTCTGAGAAAAAGTGTTCATCAAAAGTTAAAAGGCCACAGTT
 ATCACTTTTCTACCATCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGAGTCTGACTTTGTTTCTCATTCAGTTTGGGAGGAAAGGACTGTGCATTGAGTTGGT
 TCCGTGCTCCCCCAACCAATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
 TTTTATCACTCTATTATTGTTGTTATGTTTCTCATTTGTTTGGGAGGAAAGGACTGTGCATTGAGTTGGT
 CGCCTTGTCTTACAAAGCAACAGGTCCTTCTTGGCAGCTAACATGTACGTATTTCTGAATATTAAATA
 GCTGTACAGAAGCAGGTTTATTATCATGTTATCTTATTAAGAAAAAGGCCAAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRVNSQYHFTDEY
LECVSKYTEQLKPFQGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLECPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLP SNVCNDEMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDI SDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
 GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
 GCAACTTACAGCTGCACCGACAGTTGCC**ATG**AAGTTCTAATCTCTTCCCTCCTCCTGTTGC
 TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
 AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
 AGATTGGTTCTTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGC
 AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAGGCCACCACAGA
 AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
 TGCTCTGCCTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
 GACAGTGAGCACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC
 CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTGTGCTCTC
 TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCCTTACCCAGGCTTAGGCTT
 AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGC
 AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPDHFKNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

[illegible]

AATGCTGTCTTAGTACTTCGCCTGACAGTTGTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGCATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCAACAGAGTTCTCAGGATTAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGGCTTTTAGAAAGTTAGAATAAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAAAA

101/330

FIGURE 101

MAVLVLRLTVVLGLLVFLTCYADDKPKDPDDSGKDPKPDFPKFLSLLGTEIENAVE
FILRSMRSTGFMEFDDNEGKHSSK

0909/27.4.1997

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACTTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTCTGTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCCTTCATGTGGCAGCAAGTTTTTCGAGCCCACCTGGAAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCATGCGT
 CTCTAGGAACCTGGTCAAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCGAGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLLQLLVLLLTPLPHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELF SQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSM DVVVCTLVLC SVQSPRKVLQEVRRVLRPGGVLF FWEHV AEPYGSWAFM
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLP LRG T

103/330

FIGURE 104

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGACCCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGCCATTGCAGCTATAAACAGCATTCAGCACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCATAAATTTTGAAGGAA
 AAGTAAAGGAGGATCTTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCACAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTCAGCCTCTACTAAAGTTGTCTCCGTGGAGCAGGAAACCAAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAGGAAAGAAATTCGTAAGCTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGTGCAAACTGACGGAATGGAAACGACAGAATATAACTA
 ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGGCT
 GGTCAGCATCACAACACCTCCTCTGCTTATCGATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCGCCACCTTGGTTCAGTGCTGGA AAAACGATATTCACCTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAAACAGGCAAAATTCACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGA AACAGAATTTGAACGTGAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGTCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGA AAAAGATGTGTGCTAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGTGTAATGACTGGAAGAAGAACTGATATGGCTAGTTTCAGCTAGCTGGTACAGA
 TAATTCAAACCTGCTGTGGTTTTAATTTTGTAACTGTGGCTGATCTGTAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINS IQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKV VIRGAGNQNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNI TNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKA AKLLHWNHGLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCCATAAATCCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT
TGCAGCTATAAACAGCATTGAGCACAACACTCGNTCCAATGTGATTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCACGCTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTTCGGGGCGGGGCTGCA
 TCCGCATCTCTCCATCGCCTGCAGTAAGGGCGGGCGCGGCGAGCCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAACATCATCATCTTGGTCTGGGCTGTGCTCTCTTCTTACTGSTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAAGCAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTTAACTTTTGGAAGGAAAAGTAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAAATCTGGGTTCACGCGCAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACCAAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
 CTGACGGAATGGAACGACAGAATATACTAACCCTGGAATAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACCTCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAACAGATATTCACTCAGTTTGTAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTGGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTTCCA
 GACCCAAACAGGCAAAATTAACCTAATCCGAAGATATACCGAGATCTCAACATAAAGTGAAA
 CAGAATTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTAATTTT
 GTAAACCTGTGGCCTGATCTGTAATAAACTTACATTTTTCAATAGGTAAAAAAGAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTGCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCTGCTGTCAATGGGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCGTCTCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTTGCCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGTCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAAGTGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCCTGGTCTCCAGTGTGCTGGATAATAAATGGAAGTATGGCTCTAA
AAAAAAAAAAAAAAAA

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FIGURE 109

MGA AISQGALIAIVCNGLVGFLLLLWVILCWACHSRLPTLTLSLNPVTPALAPVLRPHH
PRSPAMKAATCCSPEGWPWSLEPRT

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FIGURE 110

GTTGAATTCCCTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCAGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTGTGACTCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCAGTGGAA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGCGGCCAAGTGAATATAAGCCCTT
 TTCGGGCATTTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTACTTGTTATTTCAACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATCCGAGAATCATTGTCA
 GTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAAATGGGACAGATTTCTGTACATCAGCAAAGATGCATTCAAAATCT
 TGTCGAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGAGGAGTCTATGGCTTTTAACTACAATCG
 GGCATTCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACCTTTCTGTGTTTGGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAGCCCTACTTTATGGATCAAGAAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCT
 GGAAACATTTCTTCTAAGAGCCATTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCCATTCTCTCTCAAAA

MSGRDTILGLCILALALS LAMMFTFRFITLLVHIFISLVILGLLFCVGLVWLLYYDYNDL
SIELDTERENMKCVLGF AIVSTGITAVLLVLI FVLRKRRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQOMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTANGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGLKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SLSVFEQIVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQDKHSLRN
EEGLETALDALR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCTT
 AGAATAATTTGTATGGGATTTGTGATGCAAGAAAGCCTAAGGGAAAAAGAAATATTCATCTCTG
 TGTGGTGAAAATTTTTTGAAAAAAAATTTGCCCTTCTCAAACAAGGGTGTCAITCTGATATT
TATGAGGAGCTGTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCCCTGTTTGTGCTGG
TGACTCGAGTACATTCAAACAAGAAAGCCGCAAGAAGATTAAGAGGCCCAAGTTCACTGTG
CCTCAGATCAACTGGGATGTCAAAGCCGGAAGATCATCGATCCTCAGTTCAITGTGAAATG
TCCAGCAGGATGCCAAGACCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACT
CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAGGAGGGAAAATACCT
GTTCCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCACCGTGTCCAATCGTT
ATCCCTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAGGGTCTTAA
CCTACCCCTCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCAAGCGGTGAGACC
ACAAAAGCCTATCAGAGGCCACCTATTCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACACCTTGCCAAAGCCATCCCTTCTG
CTGCTTCTACCACAGCATCCCCAGACCAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCACAGCTGATCCAGGATACCA
AAGGCAAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGTCAGCCCTGGGAC
TGCAAAAATGACTTGTGCTTTTTAATTGATGGGAGCACCAGCATGGCAAAACGCGGATCCG
AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTTGGCCCTGCCGTTCCG
TGATGGGTGTGTTCCAGTATGGAGACAACCTTGCTACTCTTTAACTCAAGACACACACG
AATTTCTCGATCTGAAGACAGCCATAGAGAAAATTTACTCAGAGAGGAGGACTTTCTAATGT
AGGTCCGGCCATCTCCTTTGTGACCAAGAACTCTTTTCCAAAGCCAAATGGAACACAGAGCG
GGGCTCCCAATGTGGTGGTGGTGTGATGGTGGATGGCTGGCCACAGGACAAGTGGAGAGGCT
TCAAGACTTGCAGAGAGTACAGGAATCAACATTTCTTCATCACCATTGAAGTGTCTGCTCA
AAATGAGAAGCAGTATGTTGGTGGAGCCCAACTTGTCAAACAGGGCGCTGTGCAGAACAAAG
GCTTCTACTCGCTCCAGTGCAGAGCTGGTTTGGCCCTCCACAAGACCTTGCAGCCTCTGGTG
AAGCGGCTCTGCGACACTGACCGCCTGGCTGCGACCAAGACTGTTGACTCGCTGACAT
TGGCTTCGTATCGACGGCTCCAGCAGTGTGGGACAGGGCAACTTCCGACCCCTCTCCAGT
TTGTGACCAACCTCACCAAGAGTTTGAGATTTCCGACACGGACACGGCATCGGGCCCTG
CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCGACAAGTACAGCAGCAAGCCTGACAT
CCTCAAGCCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAAGCAGCGGGGCTGCCATCA
ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAAGCCCAACAGAGGAAGTTAATGATCTCT
ATCACCGACGGGAGGTCTTACGACGACGTCGGATCCCAGCCTGGCTGCCATCTGAAGGG
AGTGATCACTATTCGATATAGGCGTTGCCCTGGGCTGCCAAGAGGAGCTAGAAGTCAATTGCCA
CTCACCCCGCCAGAGACCACTCTTCTTTGTGACGAGTTTGACAACTCCATCAGTATGTC
CCCAGGATATCCAGAACATTTGTACAGAGTCAACTCACAGCCTCCGGAACTGA**ATTACAG**
CAGGCAGACGACCAAGCAAGTGTGCTTTACTAAGTACGCTGTTGGACACCCCAACCGCTTAA
TGGGCGACGACCGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGCTCTGTTATTA
TCTTTGGCATCATGCTTTTTCATATTCCAAAATTTGGAGTTTACAAAGATGATCAGAAGCT
ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGCTGGAGATTTTACATTTTGACAAAT
GCTTTCAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
GTGAGATTTTTAAGTTGTTATTTCTGATTGAACTCTGTAACCTCAGCAAGTTTCAATTTTT
GTCATGACAAATGAGGAATGCTGAATTAATGTTTGAAGGATGAAAAATAAAAAA
AA
AA

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FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLRPPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGGAFFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNKTHTNRSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLPLVKRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWGGTSTGAAINFALQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFNHLQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAAC TGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTTCCGGCTGCTCATCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATTGGT
 GCGCCAGGTCGCCAGGCTCCGCGCCAGATCCGCCCCACTACAGTTTTCTCTGACTCTAAT
 TGATGCAGCTGGACACCTTGCTGATTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGCTGGGGTGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGCGGCCCGAAAACCTCC
 TCCAGCCTTTAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGAACACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCTACTTTGAGTACTTGGT
 GAAAGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAAC TACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCATGCCAGTCTTCCAGTCCCTTGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTGCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGATCCACCCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGCGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGT
 GAAATTTAGAAAAACACTGTTAGTTGCGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTACCTCCAAGTTGGCATTACTGGGACAGGTTTTCT
 AGACTCCTCATAACCACTGGATAATTTTTTTATTTTATTTTGGAGCTAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHGGAPGPDGSAPDPAHYSFSLTLLDALDITLLILGNVSEFQQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLLWVQMYKGTVSMPVFQSL EAYWPGLQSLIGDIDNAMRTFLNYTIVWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKL DNRMESFFLAETVKYLYLLFDPTNFHNNGSTFDVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

AAAGTTACATTTTCTTGGAAACTCTCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTCT
GGCAGAAAGGAGGGTGCTTCGGAGGCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
ATTGAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTG
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCTGGAGA
AACAGTGTACTATTCTGTGCAATACACAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTTCCTGAGTGTGATGTCAGTGTGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAATCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTTGGCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
CATTCGTGAAGGCCATTGGGAGTCTACAGCGCTTTAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCTCTGGAGTCTGCCCTGTGTTGCCCTTGTGGCTTACATGCTGATCCTTG
GGTCGTGCCACTGTTCGTCTGGAATAAGGGCCGGCTGCTCAGTACTCCTGTGCCCCGTGG
TGGTCTCCAGACACCTTGAATAATACCAATTACCCCGAGAAGTTAATCAGCTCAGAGAAG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCTGAGGAACCTCCTCAGGGCCTGGAT
CTCAT**TAG**GTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG
TGTTTCTGGAGAGCAGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGGCCACACTGAAAATGGGATGTGTCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGACAGGAGAATGCAAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTCT
TGTGGTGAAGATACAGAATTCAGCAAAATAAAAAGGGCCACCTTGCCAAAAGCGGTAAAAAA
AAAAA

FIGURE 117

MQTFTMVLEEIIWTSLFMWFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHL LMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSL TEGPECDVTDITATVPYNLRVRATLGSQTS AW
SILKHFPN RNSTILTRPGMEITK DGFHLVIELED LGPQFEFLVAYWRREP GAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLV LALFAFVGFM LILV
VVPLFVWKMGRL LQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGACCTGG
GGCCCCAGTTTGAGTTTCCCTTGTTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTNNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**TGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAAC**T**GGTGTGCTGCGAGAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGC GGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCCACC**A**CTTTAACGTGCTCGCCTTCCCCTGCAACAGT**T**TTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTACC**G**GTA**C**TGGTGGCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGA**A**CTTCTGGAAGTACCTAGTAGCCCCAGATGAAAAGG
 TGGTAGGGGCTTGGGACCCA**A**CTGTGTCAGTGGAGGAGGT**C**AGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTAT**TAA**CCACCGCGTCTCCTCCTCCACCA
 CCTCATCCGCCCACCTGTGTGGGCTGACCAATGCAA**A**CTCAAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTCCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGAA
 AAATCTAGTATTTTGATTATTTGAATCTTACAGCAACAATAGGA**A**CTCCTGGCCAATGAG
 AGCTCTTGACCA**G**TGAATCACCAGCCGATACGAACGCTTGTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGCTTCTGTAA**A**CTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTT**T**TGCATATAAACCAAAAAATAACTTGTATCAAT
 AAAA**A**CTTGCA**T**CCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCCCTCTGATATTATTTCTT**C**ATTACAAAAGAAATGCAAGTTCATTGTAA**C**ATCCA
 AACATACCTCACGATATAAAATAAAATGAAAGTATCCTCCTCA**A**AAA

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLSEKYRGVSLSLVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFCPNQFGQQEPPDSNKEIESFARRTYSVSPFPMFSKIAVTGTG
AHPAFKYLAQTSKKEPTWNFWKYLVPADGKVVGAWDPTVSVEEVRPQITALVRKLIILKREDL

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC
 TGCGCCCTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGGCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCAGAGAGGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTCAAGGGTGACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACCAGAGGCC
 TTGGTTCGTCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGCTGGGCATGTGGGGAC
 CTAACCTCCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGCGCAGCATCTGGACCAAGCTCCAATACAACCAGCAGTTCCTGTCTGCCATG
 ACCCCATCAACATCCAGTTTCACTCGGGGACAAACGCGAGCCCCAAGGGGGCCACCCCTCTCC
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTCCTGGGTTCGGTGGCAG
 GCACAATGATGTCTGATGTACGGTGCCACCCCTCATCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCCACCTTCCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACACGCGCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCTATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTGTCTTATGGAACCACAGAGAACAGTCCCGTGACATTTCGGCAGCTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCTGCAATTCGGCTGAAGGACGGGGAGGAGACCCAGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGAGCCCTGTCTGGCCGGTTGGCTT
 GACTCTCTCTGTGCAGAAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCAGCTTC
 TGAGCCAGGCACATCAAGTTCAGGAATTGACTGAACCACTAAGAGCTCCTGGATGGGTC
 CGGAACTCGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCCACATTCCCCTGTCTGCTCTGTGATTGGCATAAAGAGCTTCTGTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVF PKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQTSTGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMCMY GATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENS PVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEFQKT EEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGENIYPAELEDFHHTHPKVQEVQVVGVKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGGCCATGGACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGC GGGGTTGCGGTTGCGGACTCCCCGGCAAGAATGACCGCGGCCCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCAACGGCGTGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGCTGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTACGCTCAGTGCTCTGTGTGCCAGGGTCCCGCTGTAACT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCCGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTACCACCTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAAAACCCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCCGGATGAGGAGCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAC
 CGCAGCAATTACGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGCTACTGT
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC
 CAGTATCCCCAGTCTCTGCTGCGCTGGTTGCGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACAGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTGCGCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGQALECYSCVQKADDGCSFNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNALNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAFVRPTSTTKPMPAPTSQTPRQGVHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLAVAAGVLL

[illegible]

FIGURE 128

AAACTTGACGCC**ATGA**AAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCCTGGGTGGTCCTGAGGAAGAAAGCACCATTTGAGAATTATG
CGTCACGACCCGAGGCGCTTTAACACCCCGTTCTTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAAGTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT**G**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTCCATCCAAA

00089727-11801

FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
 FLNWHALFESIKRKLFPFLNWDAFPKLKGLRSATPDAQ

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

FIGURE 130

CAGTTCGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACCTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCATATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCGTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

131/330

FIGURE 131

MGVEIAFASVILTCLSLLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

FIGURE 132

GGGGAATCTGCAGTAGGTCGCCGCGCATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCCTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCCTTGGACGTTGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCAGTG
 GCCATGGAAAAAGAAAACCTCTACAGCATATTTCCGAGGATCAAGGACAAGTCAGAACGAG
 ATCCTCTCATTTCTTCTGTCTCGGAAAAACCCAAAACCTTGTGTATGCAGAATACACCAAAAAC
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAATACAAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACCTGAACATATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCACTTTTCTTAAGACCAATC
 ACAGCTGTGCGCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTTTGGAGCAGAAAATTCGTATTGGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTCTCTTTTGTAAAACCAATAAATCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLP
SAQGRQKESGSKWKVFI
DQINRSLENYEPCSSQNC
SCYHGVIE
EDLTPFRGGISRKMMAE
VVRKLGTHYQITKNRLY
RENDCMFPSRCSGVEH
FILEVIGRLPD
MEMVINVRDYPQVPKW
MEPAIPVFSFSKTSEYH
DIMYPAWTFWEGGPAV
WPIYPTGLGRWDL
FREDLVRSAAQWPWK
KNSTAYFRGSRTSPER
DPLILLSRKNPKLVDA
EYTKNQAWKSMKDT
LGKPAAKDVHLVDHCK
YKYLNFNFRGVAASFR
FKHLFLCGSLVFHVGD
EWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQ
FVKANDDVAQEIAERG
SQFIRNHLQMDDITCY
WENLLSEYSKFLSY
NVTRRKGYDQIIPKML
KTEL

CACCCCTCCATTCTCGCC**ATG**GCCCTGCACCTGCTCTGTACCTGCTGCCCTGCCTCTT
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
CCGACGATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAG
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTCAG
AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGCAGCTGGTGATGCGGTACTGGAGCC
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTT
GACTATGCTGAGCTCATGGGCCTCAAACAGTATACTACCATGTGCTGGGGCTGGGCAGCC
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCCACTGCGCCACCCAGTGTGTG
TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCTGGGCACGGACCGTCTCCTCCTTGC
TTCCTCCTTACCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCCTCTCCCACTGAATTCTAAATCCTTAAC
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTTAAATTCTGAGTTTCAGCCA
CTGAACCTCAAGGTCCACTTCTACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
TTCACCTCTCCCTGGCAGCTGTTACTTGCCCTCTGCGCCTCAGGGGTCCTTCTGACCCGCT
GGCTTCCACTCCAAGAGGTGGACACGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
GGCCCCAACCTTGCTCACCATCCCGGCCCTAGTCTCTGACCTCCTTAGGCCCTGCTCT
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCTGCTCTTAACTCGATGACTTGGGGCTC
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAAATAAAGTCAGCCTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHVPVCVELLTVLWVPTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAACTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAATGGAGCCTCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAACGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGCCAAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTCTTTATGTT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAACAGTGTGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCACTGCAGTGGGTGGGTTATATAA
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAACCCATCAAGTTT
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTCATATTCCAGAAGA
 CACAAATCTTTTCTTCTATATAGAATCCATTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTCTGCTAAGGAACACC
 ACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGAAAATTTCATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTTTGTCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAACAATGTAGAGTTTTATTATTG
 AACATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTTCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAGAATTAAGCAAGAAAATCTGAAAA

FIGURE 137

MASALWTVLPSRMSRLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVGICLNLKVN IHIPEDTNLFFLYRIHL DVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAG**ATG**AAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACT**TAA**ACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCCTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPISQLDALVKEKKLQGKGPGGPPPKGLMYSVN
PNKVDDLKSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

139/330

CAATTCTGAAACTAACTCGTGCAGAATTGACCTTTGAAAAGCATTGCTTTTTACAGAAGTATA
TTAACTTTTTAGGAGTAATTTCTAGTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAATTCCTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
GAATTAAGTAGATTGAGTCTCCAATTTTATGTAAAGCTTCAGAAGAACTGGTTTGTTACATG
CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCGGTTGCCAACTCGTCCCACTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCCTTACAAGAAGCCAAATTAAGCAAGAGGGA
TTGAATCCGGATTGGAAGCTCCAGCCCTTCAACCTCGGGTGGATTTTCTCCAGCCTCCAAGCC
ATCATCACCAGAGAAGTAAAGCTGAAGAGAAATCAACAATCTCCATTAATGTGAAGACAG
TCAAAAAAGAACCTGAGGATGACACAGCGCTTCCAAAAGCCCTTACAATGGTGTGAAGAAA
GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAGTCGATCGAGGTCAAGAACACGATCAGC
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
TCATAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAGGGGACATCATAGGGACAGCGGTGAACGATCTCGCTCCTTT
GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACCTTTCTCTCCTTTGAGCCTGCATAGTTCTTGTTTTGCCATCTACAGTGTGATGT
ATGGACTCAATCAAAACATTAAACGCAAACTGATTAGGATTTGATTTCCTGAAACCCCTCA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT
ATACATCTAAAATTCGCAGACACTGTTCTATTAAAGTGGTTATTTGTTTAAATGATGGTGAAT
ACTTCTCTTAACACTGGTTTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT
CTTGTTTTTTCTAAAAA AAAAAAAAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRVKALQEAQLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSHSESPPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKRSRSQ
SKSRDHSDAAKKHRRHERGHHRRDRERSRSFERSHKSKHHGGSRSGHGRHR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATATTCGGGTCANAATTGNCCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAGGGATT
GAATCCGGATGGAACCTCAGCCCTTTCAACCCTGGGTGGATTTTCTCTC

GGACACGAGGCCCTCGTGCCAAGCTTGGCAGCAGGGGTGACCCGCTTCTCGCACGCGTC**ATG**CGC
GGTCTCTGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCTCATGCACAGGCTGGCGC
CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGATACAAGCACCCG
TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGAAAGAGCGGTG
GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGTTCCAGCTGG
AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCGCGTCTTCTCTGGAGTACCAAGTGG
TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTACAGAGGCCCTACTACTACAT
GCTGGGACACGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
CCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTACAGCGCCGAGGAGGGGGGTGAGCGC
TCTGTCTGCCTCACCTTTGCCTTCTCTTCTCTGCTGCTGGCCATGCTGGTGCAGTGGTGCG
GGAGGAGACCCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTCTGTGGCCAAGCTGGCTATCCGCGTG
GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCCTTCTCACTTCCCAGGCGCTCGGCTCTGC
CCAGACCCACCGGAGCGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
ACACCAGCTTCTGTCTCCCTGTTTATCTGTGGCTCTGGACAAAGCCATTGCACGGGAC
TTCCTGCACACAGCCGCCGTTTGGGGAGACGCGTTTCTCCTGCTGTCCGATTCTGCCTTCGA
CTCTGGGCGCCTCTGGTTGCTGGTGGTGTCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
GAGCTTGCAGTACCTGACGCCGCTCATCTCACCTCAACTGCACACTTCTGCTCAAGACGC
TGGGAGGCTATTCTGGGGCCTGGGCCAGCTCCTCTACTATCCCCGAGCCATCTCTAGCC
AGCGCTGCCCCATCGCTCTGGGGAGGACGAAGTCCAGCAGACTGACGCGCGGATTGCCGG
GGCCCTGGGTGGCCTGCTTACTCCCTCTTCTCCGTGGCGTCTGCGCTACCTCATCTGGT
GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACAGCACTTGGCA
GGCTCC**TAG**CTGCCTGCAGACCTCTCGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
GGCGTTCCCTTACCACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
GAATCTGCTCTCTGGGCCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
TGCCAGGTTTGTAGTGGCAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
GATTTTAA

MAVLGVQLVVTLLTATPLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCLPTTVDALVLRFFLEYQWVFDFAVYSGGVYLFEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTIVRILYFSAEEGGERSVCLTFAFLFLLAMLVQV
VREETLELGLPEGLASMTQNLEPLLKKQGDWALFPAKLAIRVGLAVVGSVLGAFLTFFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLLWLVLCLLRNLACTRPHLQAYLCLAKARVEQLRRREAGRIEAREIQQRVVRVYCYVT
VVSILQYLTLPLIILNTLTLLTKLGGYSYSLGAPLLSPDPSSASAAPIGSGEDEVQQTAAIRI
AGALGGLLTPLFLRGVLAYLWWTAAACQLLASLFLGYLPHOHLAS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGNTTGGAGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTATTAACGTGGCTT
 AATCTGAAGGTTTCTCAGTCAAATCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGGCTTAAGGAGGC
 TTGGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACATGCTGGGAGAATGAAGG
 CGCTTCTGTGTCTGGTCTTGCCTTGGCTCAGTCTCTTAACATATTGACAAATGTGGGCAACCTGCACCTTCTCTG
 TATTGAGAATCTGTAAAGGTGCTCCCACTACGGCTGACCAAAGATAGGAAGAGCGCTCAAGAATGECTG
 TCCAGACGGCTCTGCGAGCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGSCCTAGACAACCTGCCTACGTGTCTCTGGCAGAGGACGGGCAGCCAGCAATCAGCCCA
 GTGCATCTGGCCGGAGCAACCGAAGTGGGACGGCCCTTGGAGATCCACTATTAGAAAGCAGATCATTAA
 AAAATAAATCGAGCTTTGAGTGTCTTTCGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACGAGG
 GCAGGGAAAAATCTGAAAACACCACTGCCCTGAAGTCTTTCCAAGGTTGTACCACTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGATAGATCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCAAAGGTCAACGGGATGGACATCAGCAATGTCCCTACAACCTACGCTGTGGCTCTCTGGCGG
 CAGCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGAGCAGGAACAATGGACAGGCCCC
 GGATGCTCAGACCCCGAGATGACAGCTTTCATGTATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACCTGGTGGCAAGGTGGATGAGCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGGAAG
 TGGCGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTCACCTCGTGTGTCGCCCGAGGTTGGCAGCGGAGCC
 CTGACATCTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGTCTCCCGAGGCCAGGGGAGAGGACCAACT
 CCCAAGCCCCCTCATCTCAATTAATTTGTGATGAGAAGGTGGTAAATCCAAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTATCAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTGTGGAATGTGGATGGGGTTCGAATGACA
 GAGGTGAGCCGAGGTGAGGCAGTGGCATTATGAAAAGAACATCACTCCGATAGTACTCAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCCACACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTTCATGTGGCTGGAATTACCACGGTGTGTGATAACTGTAAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATGTAGGAGGTTATGAAGATACATGGAACACAACTTTT
 TTTTCATCAAATCCATTTGTTGAAGGAACACAGCATACAATGATGGAAGAATAGATGGGTGATATCTTCTCTG
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGTGGAAGACTGCTGAAGAACTTARAGGAAGA
 ATTACTCTAATATTGTTTCTTGGCTGGCAGCTTTTTCATAGATCAATGATGGGTGAGGAGAAACAGAAAAA
 TCACAAATAGGCTAAGAAGTTGAAACACTATATTTATCTTGTGAGTTTATATTAAAGAAAGAAATACATTGT
 AAAAATGTCAGGAAAAATGATCATCATTAAGAGCCAGTTACACCTCAGAAAAATATGATTTCCAAAAAATTA
 AAAACTAGTACTTTTTTTTCAGTGTGGAGATTTCTCATCTCTACACATCTGTATATTTTTTCTATTCAAT
 AAAAGCCCTCAAACAACTAAATGATTGATTGTATACCCCACTGAATCAAGCTGATTAAATTTAAATTT
 GGTATGTGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTAAATTTACAGCTAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTGCTTTCATCAACAGAATAAATATTTTTCAGAGTTAA

MKALLLLVLPLWLSFANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
 APSPEVSAATISLMTDEPLDNFAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
 FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVD
 SESLSIRLVGGSETPLVHIIQHIYRDGVIARDGRLLPGDILKVNMGDISNVPHNYAVRL
 RQPCQVLWLTVMREQFRSRNNGQAPDAYRPRDSSFHVILNKSSPEEQLGILKVRKVDPEGV
 FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLRYGSPESAALHIQASERRVHLVVSQRVQRS
 PDFIQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHRE
 WDLPIYVISVEPPGVISRDRIGTKDILLNVGDVELTEVSRSEAVALLKRTSSSIVLKALEV
 KEYEPQEDCSSPAALDSNHNMAPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
 GGYEYNGNKKPFIKSIVEGTPAYNDGRIIRCGDILLAVNGRSTSGMIHACLARLLKELKGR
 I
 TLTIVSWPGTFL

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCA**AATG**GTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGGTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTAC
CCATTGAGAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCCGTGCTGGAGGCTGTGCAAAAGCTGGGCTCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCAATGTT**TAG**CGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACTACTCAAAGTCAAAATTAATCTTTTCCAATGCCCACTAATTTTGAGATTC
AGTCAAGAAATATAAATGCTGATTATATA

MKILVAFVLVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
 IFDYKHGYIASRVLRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
 SLIKDVDWFLGSPIEKLCKHIPLYKEVVENTHNVGAGGCACAGLGLGILGISICADIHV

GGACAGGCCAGGAACACTAGGAGGTTCTACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAAT'TACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCAAAG
 GCCGTGGGTGCTCATAACTGCTGTGCACCCAGCCACCACCGCCCATCCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCAGACCTGCTCACTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGCTGAGCTGCGGGCCAACCTCACTCTGCAGGACAGAGGGGCGAGGCCCAAGGGTGGGA
 GATGATCTGCCAGGCGTCCTCGGGCAGCCCACTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCACCTGTCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTCGCG
 AGCCAGACATCGGACTGGTTCGGTGCCAGGCTGCAAAACAACGCCAATGTCCAGCACAGCGC
 CCTCCACAGTGGTGCCCCAGGTGGTGACCAAGAAGATGGAGGACTGGCAGGGTCCCTGGAGA
 GCCCATCTCTTGCCTTCCCGCTCTACAGGAGCACCCCGCTGTAGTGAAGAGGAGTTTGGG
 GGGTTCAGGATAGGGAATGGGAGAGGCTCAGAGCGCAACAGCAGCCATGCT**TAGA**ATGAAC
 GTCCAGAGAGCCAAGCAGCGCAGAGGACTGCAGGCCATCAGCGTCACTGTTCTGTATTGGA
 GTTATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAAAAAA

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPFKGRWVLITCCAPQPPPPITYSL
 CGTKNIKVAKKVKTHEFPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
 PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCRHPANFSLFLP
 SQTSDWFWCQAANNANVQHSALTVPVPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
 FGRIGNLVEVRGRKAAM

amino acids 1-18

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAA
 CTTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCACTCCCCTGGGGAAGAAA
 CTAAATGTCACAACGGCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCCCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCACTCGCCATGTCTCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCTCCCTGGCA
 TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCTTT
 TTGCCAACAAATTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
 TCTTTTGTGTTGGAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
 AATTTTTAAATTATTTAATAAGAAAAATTTATATTAAATGATTGTTCTTTAGTAATTTAT
 TGTTCTGTACTGATATTTAATAAAGAGTTCTATTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
HYDCGNKTVTPVSPGLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLLCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGCGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCCTCACAATTTTCATTCTGTTTTCTGACTTCAAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHLEWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGPTEQHFWARL

1993-11-11

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA
 CCTCACGGGCGAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGGCCCC
 AGAACTGCCCTCCGTTTGCTCGTGCAGTAACCAAGTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCGGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGCGAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCTTTGAATACCTGTCTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATCGCCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTCGTGGGGCTGGAGGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTATG
 AACTCACAGGTGACGCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACTTGGCCCAATAAACCTCTCTTCTTGGCCCATGACCTCTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATCTCTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCCTGTCTGCTCCCAT
 GCACATGCGAGGCGGCTACCTCGTGGAGGTGGACCAGGCTTCTTCCAGTGCTCTGCCCCCT
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCCGATGGCAGAAGCTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCAATGGGACAGTGTCTCAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGTGCTGC
 TTTGACAGACTGGGGTGACACATGCATGGTGACCAATGTTGACGGCAACTCCAACGCCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAGTACAAGCCTGTTCTTA
 CCACGTCCACTGTTTACCAGCCGGCATATACCACCTTACCACGGTGCTCATTACAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACACAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGCGAGTAGTCTGCCACAATTC
 ATGACCATATTAACATAACAACCTACAACACAGCATGGGGGCCACTGGACAGAAAACAGC
 CTGGGGAACCTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTACAGACCA
 TACCAAGGACAAAGGTACAGAAACTCAAATAT**GCACT**CCCCCCCCAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGCTGGTAAAAAAAACAGATTATATATAAAATTTAAAGA
 CAAAAAGTCAAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNLYNLGMCNIKMPNLTPLVGLEELEMNGHNFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPDHLFTPLRYLVELHLHHNPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFOCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHRPRISVLNDGTNLFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLVNSTAELNLSNYSFFTFTVTETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDITDKMQTSLDEVMTTKIIIGCFVAVTLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDI PAATSAAATAAPSGVSGEGAVVLP TIHDHINYNTYKPAHGAHWTE
NSLGNLSLHPTVTTISEPYIIQTHTKDKVQETQI

[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSSLHVLFSHDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPH
QLYSAAFSKQKLSAPTCKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCAWSEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAAC**ATG**GGC
 TTCAACCTGACTTTCCACCTTTCCTACAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAAC**T**ACTTCGTGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGA**ACT**TGACAAC**T**GTCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTCGCCATC
 CTGTTCCCAACCGGAACAGAGAGAAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAAGCTGAAGGTAAAAAGT
 TTAATCAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTTGGGAC
 TGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCCAAGCAGTGAACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGCCCCCTGCCTGAAGTGGGTAATATACAATGGTCTTCCCACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGCTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCA**TGA**CCCTGGATCTTTTGGTGATGTTTGG
 AAGA**ACT**GATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAA**T**AGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCCCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCCACGAATCA
 GGACACAGTGA**ACT**TGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACACAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTA**ACT**AAATAATAATA
 TGTCTATCAAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVLTALSREQFFKVNG
FSNNYWGWGGEDDDLRRLRVELQRMKISRPLPEVGKYTEMFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSVEHNPLYINITVDWFVGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

CGTGGGCCGGGGTGC GCAGCGGGCTGTGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTC
GAGCTTCAGCTGCATTCCTCCGCGTCCGCGCCAGCCTCTCCCGCTCCGGGCCCGCGATG
GCCAGGACGTTGGTGGCGCTCGCGCGATCTCTGGTGTGCTGCTGCTCTGCCTGGCG
CCCGGCGAGGGGTGCCCGCAGGCCTGTATGAACCTCAATCTCACCACCGATAGCCCTGCCACCA
CGGGAGCGGTGGTGACCATCTCGGCCAGCCTTGTTGGCCAAAGGACAACGCGAGCCTGGCCCTC
CCCGCTGACGCCACATCTACCGTTCTCACTGGATCCACACCCGCTGGTGGCTTACTGGCAA
GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCAGCTGCCCGGGGAATTCCCG
TCTGTCTGGGTCACTCCGCTGACTGCTGGATGTCAGCAGCTGTGCCACGGGCTCTTGTG
GTCTTCCCATCACAGAGTTCTCGTGGGGGACCTTGTGTACCCAGAACATCTCCCTACC
TGTGGCCAGCTCTATCTACTAAAGACCGTCTGAAAGTCTCTCTCTCTCTCCACAGCCGA
GCAACTCTCAAGACGCGCTGTGTTTCTCTACAGCTGGGACTTCGGGAGCGGACCCAGATG
GTGACTGAAGACTCCGTGGTCTTATAAATATTCACTATCCGGAGCTTCACCCTGAAGCT
CAAAGTGGTGGCGGATGGGAAGAGGTGGAGCCGGATGCCACGAGGCTGTGAAGCGAAGA
CGGGGACCTTCTCGCTCGCTGAAGCTGAGGAACCTTCAGGACTCAAGATGTTGGGG
CCCAACCTTAATCAGACTTCCAAGAAGATGACCGTGACCTGAACTTCTCGGGAGGCCCTCC
TGTACTGTGTGCTGGCGTCAAGCTGAGTGCTCCGCTGGAGGAAGGGAGTGGCCAC
CTGTGTCCGTGGCCAGCAGCGCTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC
TGCTTCAGCATCCGGGCGGAGAATATCATCAGCAAGACATCAGTACACAAGATCCAGGT
GTGGCCCTCCAGAAACGACGGCGTGTCTTTGTTTCCCATGTGTCATCACTTATCACTGTGA
TGTTGGCCTTATCATGATGATACGACCTCGGGAATGCCACTCAGCAAAGGACATGTGGAG
AACCCGAGGCCACCTCTGGGTGAGTGTGCTGTCGACAGTGTCTGTGGCCCTTTCTGTCT
GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACCGGGCTGCTCCGCGCCCTCT
ATAAGTCTGTGCAAAATCTACACCGTCTGACGACACTCCCTCCCCACCCCATCTCAGTGTAA
CTGACTGCTGACTTGGAGTTTCCAGCAGGCTGGTGTGACCACTGACGAGGAGGGTTCAT
TGGCTGGGGCTGTTGGCCTGATATCTCATCTCATCTGTACAGTTTCAGCCACTGCCACAAGCC
CTCTCTCTCTGTACCCCTGACCCAGCCATTCACCATCTGTACAGTCCAGCCACTGACA
TAAGCCCACTCGGTTACACACCCCTTGACCCCTACTTGAAGAGGCTTCTGTGAGCACT
TTGATGTTGGGGGTGTTCCGTTGACTCTAGTGGGCTGGCTGCCACTGCCCATGCCATCTCT
CTCATATTTGGCAGATCTGCTGTCTATGGGGGTTCTCAGTTTCTCCCTCCAGACAGCCCTA
CTGTGCCAGAGAGCTAGAAAGAAGGTCTAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
ACATAGATGGGCACATCACAGAGAGAAGTGTGCATGTACACACACACACACACACACA
CACACACACACAGAAATATAAACACATCGCTCATGTCAGTGGCATTCAGATGATCAGCTCTGA
TCTGGTTAAGTCGGTTGCTGGGATCGACCCCTGCATAGAGCTGAAAGGAATTTGACCTCCA
AGCAGCCTCAGAGGTTCTGGGCCGGGCCCTCCCTTTGTGCTTTGTCTCTGAGTCTTGTG
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
AATACTGAGTGATTGAGAGTGCTTTATAAATATCACTTATTTTACGAAACCCATCTGTG
AAACTTTCTCAGTGAAGAAAGCCCTTGACGCGGTAGAAGAGGTTGAGTCAAGCGCGGCGCG
TGGCTCAGCCCTGTAATCCAGCATCTTTGGGAGCGCGAGCGGGTGGATCAGGAGATCAGGA
GATCGAGACACCTTGCTTAACACCGTGAACCCCGTCTCTACTAAAAAATACAAAAGTT
AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGCTCATCGGAGGCTGAGGCAGGAGAATG
GTGCGAACCCGGGAGGCGAGCTTCAGTGAAGCCAGATGGCGCCACTGCATCCAGCTGA
GTGACAGAGCAGAGACTCTGTCTCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPNFKLTALFLYSWDFGDGTQ
MYTEDSVVYYNYSIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFSSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKITYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

[illegible]

165/330

FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCKT

165/330

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTTCCTGTTGCTGCCTTTTGTATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCCCTCTTACCCCTCCTTCTCGTTTTCAATCATAGTGCCAGCCATTTTTGG
 AGTCTCCTTTGGGTATCCGAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATGTGCAAGGATCCCACTTCACTAGAGAAGAGATCAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGCTGATTCCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACGTGGTGGGATACCTTGCCAAAT
 GGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTCAGAGAGCCATGGTGAAGGCCGTG
 CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAGGAAGCACTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
 TGTGTCTATCAAGTATGACCCCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAACGGGA
 TGGTGACGTACCTGCTGCCAATGATGACCAGCTGGGGCATTGTCTGACGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGTC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCTGCGGGGAACCAC
 AAGGACAGGAGCCGCTCCT**TGAG**CCTGCCTCCAGCTGGCTGGGGCCACCCTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCGCGCGCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTTCGCCGAGCCGAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACCGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCCTTGTTCTTTTACAATAAGTCGTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTCTGGGGGGCGGCCACCCG
 CTCTCCAGGAAAGGCACAGCTGAGGCACCTGGCTGGCTTCGGCCTCAACATCGCCCCAGC
 CTGTGAGCTCTGCAGACATGATAGGAAGGAACTGTCATCTGCAGGGGCTTTTCAGCAAAATG
 AAGGGTAGATTTTTTACTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGGAGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGTACTCCAGGCTAACCTGAACTCCCC
 ATGTGATGCGCGCTTTGTGAATGTGTCTCGGTTTCCCCATCTGTAATATGAGTGGGGG
 GAATGGTGGTGATTCTTACCTACCCAGGGCTGTTGTGGGATTAAGAGTCTGCGGGTGAGTGA
 AGGACACATCACGTTTCAAGTACAGGCCCAAAAACGGGGCACGGCAGGCCTGAG
 CTCAGAGCTGCTGCATCGGCCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRK GME
TIMDDEVTKRFSAAELESWNLLSRTNYNFYIISRLTVLWGLGVLIRYCFLLPLRIALAF TG
ISLLVVGTTVVGYPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRRPRNGGICVAN H
TSPIDVILIASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLP PMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

FIGURE 168

GCCCCTCGAAACAGGACTCCAGCACCTCTGGTCCCGCCCTACCCCGACCCCTGGCCCTCA
 CGTCTCCTCCAGGGATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
 ACCTGGCAGGCCAGGCTGTTCCACCATCCTGCCCTGGGCCTGGCTCCAGACACCTTTGA
 CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCCACCATGCCCTGCTGCGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
 GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTCTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGG
 AGGTGTGGGCAGCCTTCGCTTTGAACCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTGGGGAGAAGAGGCGGGGCTGT
 GTGTCTGCCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTGTGCCCCCTG
 GAAGACTCTGCTCTTGCCCTCGAGAGTTCCAGCTCTCAGGGGTGGGGCCCTGAAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAGCAAGAACATGGTTCGGGACCCAGCCCTAGCAGCCTTCTCCCAACAGG
 ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTATGTGATGGGACTTCCT
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKEAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFFFKALHFYLIRALQLLRSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLTLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAAT**ATG**GCTGGTTCCTCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAATGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAAATGAGTC
CCATAATGGGTCCATCTCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCGTGCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCTCCTGTGTCTCCTGTTGGTGCCCTT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAGAAATCCCCACTCAC
TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATC**TAG**ACAGCAGTG
CACTCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYLWQLTGSAASGPKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLTTPDTPRLFAYENVI

10086727.1.1.1

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCAGATTCTCCATGGTCCCTCCT
GTGTCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTGCGGAA
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAAAATCCCCACTCACTGCTCAGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACCTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGCCATGCAGAGAAGCTAGTTCTACGGGAAGGA
ACTTTAAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCCTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGACTCCACCATCATCCCTTCCATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTGATACCCCTTGACAAAT
TTTTCATGAAATTATTCCTCTTCTGTTCATAAATGATTACCTTGCACTTAA

FIGURE 174

MKMLLLCLGLTLCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

GGCTCGAGCGTTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTACAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCA
CAGTCATTGGTGTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAAATTTTCATTGAAAAACATCAGTGA
CATTTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAAACAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCATTGCT
TGTTGGAATTCTGGAGGTCCTGTGTTGGGCTCAGTCAGATAGTCATCGGTTTCCCTTGGCTGTC
TGTTGGAGTCTCTAAGCGAAGAAGTCAAATTTGTGTAGTTTAAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAA

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
 IPATMTSLTARKACNNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMNCNSPSNSNA
 NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDFDSEENKHLR
 IHFSVFLGLLLVGILEVLVFLGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCCAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAAGCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAATAGTGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

0986727.11901

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACA CTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

180/330

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDFFYYDWKNLQLSGLICGGLLAAGIAAVLSGKCK
YKSSQKQHSPVPEKAIP LITPGSATTC

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FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
TGGCTGGGCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
CTGGCTACTCGCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCCGGGCTCC
AGTGTTTCCACAGCCCCAAAACGGAACCTGGTTTTGGGGTCACCTGGGCTGATCACTCCT
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATCCAGGGCTTACGGT
ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
GCCCCGCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
TCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGGCGC
TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGGCTCG
CACCTCCCCACTCAGGATATTGATGATTTTTTCAAGACAAAGCCAAGTCCAAGACTTTGG
ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
CTGGGTCTGTACAACCTTGCAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCC
TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTGCC
TCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGATCCTGAGGTCTACGAC
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTC
CGCAGGGCCCAGGAATGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCCTGG
CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTACTTTCTGACCCATCCACCTGTTTTTTTGAGATTGTGATGAATAAACGGTGTGTCAA

FIGURE 182

MSLLSLPWLGRLPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGLLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHASEGS
SRLDMEFHHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDEDEG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLAHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC
AGTGTGGAGAAAACTAGGCAAACACCCCTGTTTATTGTTACCTGGAAAATAAATCCTCT
ATGTTTGCACAAAAAAAAAAAAAA

184/330

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

184/330

FIGURE 185

GAACATTTTGTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCACTCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGA

186/330

FIGURE 186

MPSPGTVCLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCAACCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACAACCTCCCTGCTCCTGGCACAGCCGTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCTGCGATGTTGGCAAGAACGCCAGCTCAGAATGAACACACCCCAACGA
 GCCTCCTTGTTATAACACAGGTTACCTTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVVIIGMLVLLDFLGLVHLGQLLI FHIYLSMSEPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEELTPRPAGVVPGA

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FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGCTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCCCTCTGTCTGTCTCAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATATATGGCTG
 GGCCTTCTACATGGCTGGCTCTCCTTACCTGCTGCATGGCTCGGCTGTCAACCCTTCA
 ACACGTACACCAGGATGGTGTGGAGTTCAAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAAAC
 CCGAACTGCCTACCACATCACCATCAGTGTTCCTCGCGGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCCCTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCCCTACAGCTCCATCTTGTTTCACCCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRFSSFRSGMWLSCSEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPLGLCGKNPMVIPGNADHLHRTSIHQ
PPATNRLATHWEPCLWAQTERLCCCCFLCPVRSPGDGGPHDVFTSLPSPDCQLGSRRLLETTCL
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

AACCTGGAAGGAAAGAAAGAAAGGTGACGCTTTGGCCCCAGATGTTGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTCTATTCTGTGTCATCTCCCTCACTTAAGTCTCAGGCCGTGTA
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGACCCTAACCATCTGTGCTTCTG
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCTCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTCAGCCAGTATTAAATGTCCTCTCCCTTCCCCGTGCCCGGCCGTAGATTGAG
GACATTGCGCCCTGTGTGCCACCAAACAGGACTTCTCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGCTCTGTTCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACAAA
GGGAAGCAACAGGAACTCTGCAACTGGTTTTTATCGGAAAGATATCCTGCCTGCAGATGC
TGTTGAAGGGGCAACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTCAGGTTGTGAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATCTGATTCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCTCCCCGTAGCCCTCTCCAGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATATATGCC
CATGCCACCAAAAACAATAAAACAAATTTCTCTAACACTGAAA

192/330

FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLFSPPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

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GTAGCGCGTCTTGGGTCTCCCGGTCGCCGCTGCTCGCCGCGCCCTCGGGTCTGGAGGCCAGAGGACGCTCA
CGCG**ATG**TCAGGAGCATCAAGGCTTTGATAGTTGTTCTTTGGAGAGGCAATCGGACTGATGTTTCTGATCCT
GGGATGTCCTTTCCAAATATACAAACAAATCGGCCCTCTGTTGTATCTTTTACATCTCTTCCACATATCC
ATACTCGATACAGAAGATTAGTGATGATACAGATCGTATGAGTACCGGTTGTAAAGAACTTGGCATCTTTC
TTAAACAGGGCATGTGCTGTGACGTTTGGACCTCCTATTGATTTGCGAGACAGCATCTGATTGAGTGGGGA
CGTTTGTGACCTTTGTTCTACAGGAAACAGCATGATCTTTCGAATATATACTAGGCTTTCTTGGTCTTTGGAA
CAATGACGACTTCAGTGTGCGACAGCTG**GTG**AAAAGAAATATCAACAAATCTCAAAATGGACTCTGCTGATCT
TTGTGGCCATTCACGCGACAGGAGATGGGGCAGTTAATGCTGAATGGTATGACAAGCCTCTTGGGGGATTTTA
GGTGTCCCTTCTCACTTTTATTGTAAACATACTATTATACAGAGACTGCTGGAAGATAAAGAGATTTCCT
CTTTTGGAAAGAACTTGACTGATTTCACACATATCTATAGATATGCTTTTGTGGTGTCTCGTGAATTTAAATAT
TTATGTGTGTTTCTGTGTAGTTGATTTTTTTTGGAAATCAATATGCAATCTTAAACACTTTTAAATGATCAAT
TTTGCATTTGTTAGGAATCGAAATTCGCCGGCTCTATTACTGCTGCAAGTACATCTTTTCTTAAATATTTT
TAGCCTCCAAATTTATCAAAAAATATAAAAAAATAGTTTTCAGTCAAGCAGATGACATCTCCCAATGTTATG
CAGACATACAGACGGTTGGCATATGTTATAGACTGTATACCTAGTCAAAATATAGCTGCAATTTACCTCCAGAG
GGGCGAAGTGTAAATGCCATGCCCTCGTTAAGGGTGTGTTGTTTCTACTGTGACAGACATGTTTGTGGATGT
AAAAATTTTATGAAATTCGTACAGAGAGAGTGCTTCTCTCAATTTGTAGAAGAAATTTATGTAAACTTTA
AGGTAAAGGTGTAAAAACATTTTGGATAGAGTTTATTTATTTGTTATATATGTAGAGTGAAGTGGCAATGT
GGGAAGAAATGACATTTGAATTCGATTTTGTGAATCTGTTCTTATTTTAAAGTGAATTTGTGATCTCCATAT
ACCTTCTCATGTTTACCCTTTGTTAAAAAGGACATACATGGACCACTACTGAGGGACAGTTGATGTTTGG
ATCATATATGGCGAAAGAACTCTCTGCTCTCTCTTTGACTTATTTGGTATATGTTATATATATACATAAAA
TAACTTTCAAATATAGTTTAAATACACTAGAAGTGTATCACTACCTGGAAATTAATGCTATGCGCTACATTT
CAGAGTGCCCTCCCTCGCGAAGGCCCTGCGATGATTACCAAGTAACTTGTAGCTTCACAGATAAATCATGCA
TTAAAGCTTTAAGATTTAGACATGGAATAGTAGTTCTTATTTCTAAAGTTATATCATATGTAATTTAAAG
TTTTTTAAAGCAGTTTCTGTATACCTTGAACTGTTTGATTTGAGTTTATCATGATAGATCTGTGTTGTT
CTTTATAAAGGCATTTGTTGTGTGAGTAAATCAAGTAGCAAGTACGATATATAGCAGCTTCAGAAAGAT
ACCTGACCAAAAAATTCAGATACACCGGCAATCAATTTACAGTGGTCTTTTACATCATATTAATATCAGGA
CTTTTTCAGGATGGGTTATAAAAAATCAAGTGGTCTGACAGTTTGTTAAGATATTTGTTGTATG
TTTATTCAGTATATTCATCAAAAAATTTTCGCCATCAGCGAAAATCAGTAATCATGACAGCTGTCTGTCT
TTTATAGAGTTTATTTCTCAGAAAAATGGGAATAAATTTGGGATTTGTCAGTCTTTTATTAAGATAGCTCA
CGCGACAGGTTTATTGCTCACTTACAGGCTAGCTTTAGATATGAGATCAGGGGAACGAGGACAGAAATCG
GGGTGTGCGTGAGCCTTCCCATCTGGAGGCTGAAGATGGCTTGTGGTATATAAATGTCAGATTTCAAGAGGAA
GGTGAGGTTACACATGAGTTAGACAGCTGGTGACAGACTGGGAAGCTCTTGTGCTGTGATCTAGCTGGAATTT
TTTTTTCAGGAAGATGCACTCTCTGCTGCTCCCTATTTCCTGTCGAGTGCAAGTCAAGTGCAGCTGCTACTG
TTTTATCCACTTGGCCACAGACTTTTCTACAGCGCGTATATTTCTATATACATAATGACTGATGGCAGCAAT
GTGTCTTGACCTGTATACAGCTTGACATAGTGTGCTCTGATTTTAGGCTAGTTGACTTGAGATATGAAT
TTCCATAGAAATGACATGATACACATACCACTTCTCTATGAAAGAAAACCTTTGATGATGAACAATAA
AGTTTATAATCTCAATTTAAAAAAAAAA

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

194/330

[illegible]

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTELHLEHNDLVKVNFAHFPRLISLSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAYAFHLCEDGAEPSTG
HLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
LEGALVIINEYGSCCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCCGTTGAGTTCCCGCGGACAAGATGG
TGTCACTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGAA
CTCGTCTTGGCTTCAGGAGCCGGATTCCGCCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCTGCCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGGGGCCGCTACGCTTCCACGGGCCGGCGCGCTTGAGCCTG
GGCCCCGAGGACTGCGCGGACCCGTCCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCT

MGVLGRVLLWLQLCALTAQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLPLDGLVLASGAGFGVSDVGSGLDCGAGEPAVFRSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPGLSVGPEDCADPSGCVCGNAEAQPWICALLQP

[illegible]

FIGURE 201

TTGAGCGCAGGTGAGCTCTCGCGGTTCCGGGGGCGTTCCCTCCAGTCAACCTCCCGCGTTACCCGCGGCGCGC
CCGAGGGAGTCTCTCCAGACCTCCCTCCCGTTGCTCCAAACTAATACGGACTGAACGGATCGCTGCGAGGGT
GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
AACTGATCAAGTACTTTGAAATGACTTCGAAATTTATCTTGGTGTCCTTCATACTTGCCTGCACTGAGCTTTTC
AACCACCTTTCTCTCCAATAGACAGCAAAAGGTTCTACTAGTTCTTTTGGATGGATTCCGTTGGGATTACT
TATATAAGTTTCCAGCGCCCATTTTCATTATATATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
TTTATATCAAAAAACCTACCTAACCATATATCTTTGGTAACTGGCCTCTTTCGACAGAAATCATGGGATGTTGTC
AAATGATATGTTGATCCTATTTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTTCCAAGTTT
GGGAGAGAGCGACCAATATGGATCAAAACAGAGGGCAGGACATACATAGTGGTGCAGCCATGTGGCCCGGA
ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
AGTTGCCAAAATTTGTTGAATGGTTTACGTCAAAAGAGCCCAATAATCTTGGTCTTCTCTATTGGGAAGACCTG
ATGACATGGGCCACCAATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCAATTCAGATATTGACAAGAAAGTTA
GGATATCTCATACAAATGCTGAAAAGGCAAAAGTTGTGGAACACTCTGAACCTAATCATCACAAGTGATCATGG
AATGACGCACTGCTCTGAGGAAAGGTTAATAGAACTTGACCAGTACCTGGATAAAGACCCTATAACCTGATTG
ATCAATCTCCAGTAGCAGCCATCTTCCCAAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAACTACCGCT
CATCCTAATCTTACTGTTTACAAAAAAGAGAGCTTCCAGAAAGGTGGCATTTACAAATACAAACAGTCGAATTCA
ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTTTACAGAAATAGTCAGATGACTTCTGTTTAGGCAACC
ACGGTTACGATAATGCGTTAGCAGATATGCATCCAAATATTTTAGCCCATGGTCTCGCTTCAGAAAGAAATTC
TCAAAAGAGCCATGAATCCACAGATTGTACCCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
CAATGGATCATTTCTGGAATGCTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
CTATACTCCTCCCTGGTAGTGTTAAACAGCAGAAATATGACCAAGAGGGGTCTACCCCTTATTTATAGGGGCTC
TCTCTTGGCAGCATTATAGTGATTGATTTTTTGTAAATTTTCATTAAACATTAAATTCACAGTCAAAATACCTGC
CTTACAAGATATGCATGCTGAATAGCTCAACCATTTATACAAGCTTAATGTTACTTTGAAGTGGATTTCGATA
TTGAAGTGGAGATTCCATAATATGTGAGTGTTTAAAGGTTTCAAATCTGGGAAACCAGTTCCAAACATCTGC
AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACACACACACACAGGACCAAA
ATACTTACACCTGCAAAGGAATAAGATGTAGAGTATGCTCCATTTGCTACTGTAGCATAGGGATAGATAAG
ATCCTGCTTTAATTTGGACTTGGCGCAGATATATGATATATTTAGCAACTTTGCACTATGTAAGTACCTTATAT
ATTGCAATTTAAATTTCTCTCCTGATGGGTACTTTAATTTGAATGCACCTTTATGACAGTTATGTCCTTATAAC
TTGATTGAAATGACAACTTTTTCACCCATGTACAGAAATCTGTTACGCATTTGTCAAACTGAAGGAAAT
TCTAATAATCCGATAATGAACATAGAAATCTATCTCCATAAATTTGAGAGAAGAAGAGGTGATAAGTCTGA
AAATTAATATGTGATAACCTTTGAACCTTGAATTTTGGAGATGATTCCCAACAGCAGAAATGCAACTGTGGCAT
TCTCTTGCTTATTTCTTCCAGAGAACGTGGTTTTCATTATTTTCCCTCAAAAGAGAGTCAATACTGCAGAC
ATTGCGTCTAATAATATTTGTTCTCTCATAAATATTTGTGATTTCTGATGAGTCATATTAATCTGATTTTCA
TAATAATGAAGACACCATGATATACCTTTCTCTTAATAAGTACAGAAATGGCCTGAATAGAGACACCCAGGCA
CCATCTCAGCAATGTTTCTCTTGTGTAATTTTGGCTCTTTGAAATTAATCATTATTAATTAATACATTAA
AAATCAAAATGGATAAAAA

CCGCGGCTTACCCGCGGCGCGC

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
ITNQAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPPVISDIDKKLGYLIQMLKKAKLWNTNLNLIITSDHGMTQCSEER
LIELDQYLDKDHYTELDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGGATTTCGCTCCCACGGCGGGACCTTTGTAACTGCGGGAGGCCGAC
GACAGGCCACCTTCGCGGGCGGGAGGCAGCGGGGTGAGGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
CCAGATCCAGAGGCCAAGGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGAGGGGCC
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCATTCACGGTCGTGGGAGACGA
CTACCATGCTGGAAATCAACTACAAGAAATGGGAGAAATGAAGAGGAGGAGGAGGAGGAGG
AGCAGCCACCACCACACCACTCTCAGGCAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
CCTGCCCTTGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCCACAGTTCTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCTTGGACATCTGAAGATCATCAGCCCGACAAGAATAACTATGCTGCCATC
GTATTCCACTACATGAGCATCACCACTCTTGGTCTTTTTATGATGGAGATCATCTTAAATT
ATTTGTCTTCCGCTGAGTTCTTACCACAAGTTGAGATCCTGGATGCCCGTCGTGGTGG
TGGTCTCATTATCCTGGACATTGTCTCTGTTCCAGGAGCACCAGTTTGAAGCTCTGGGC
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTCAGAACGGCAACTCTTAAGTTAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGACTTGATGAGTTTGTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCATGAGGAATGAAAGAAATCCGACTTCTACTCT
CACACAGCCACCGTGAAAGTCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
CAGGCTGGCATGTTACTGGGCTGGTGTTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
TCAATCTCAGATTACAATCACACAGAGCATCTGCCTGTTTTCAATCAAGAGAACAACAAAC
AAACTCTATAAGATATTCTGAAATATGACAGAAATTGACAATAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVPAERMSKFLRHFTVVGDDYHAWNINYYKKWENEEEEEEQQPPTFV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMRLKLFSSSHRFQV I I CLVVL DALLVLAE LLDL
KI IQPDKNNYAMVFHYMSITILVFFMMEI I FKL FV FRLSSFTTSLRSMPPVVVVVS FILD I
VLLFQEHQFEALGLLILLRLWRVARIING I I ISVKTRSERQLLRLLQMNVQLAAKI QHLEFS
CSEKPLD

POLYMER LETTERS

FIGURE 205

CGGCTCGAGCTCGAGCCGAATTCGGCTCGAGGGGCAGTGGAGCACCAGCAGGCCGCCAACAT
GCTCTGTCTGTGCTGTACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCAGTACATTTTG
 AGTCGAAGGGGGTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCCACCTACCCGAGTGGAGCCAGAAAATTGTACAGCTGGAGATAAGGACCT
 TGTATGGGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAAGTATCATGAGAAGAGCTGA
 GGCTGGGTGTTTAAATTTTGGACAAAAAGAAATATGGACGCATTGACGGCCAGGAGATCATG
 CAGTCCCTGGCGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCAAGAG
 CATGGATAAAAAAGCCGACGATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCCTCC
 ACCCGGTGGAAAAACATCCCCGAGATCATCTCTACTGGAAAGCATTCACGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTTACAGTGGAGGAGAGGCAGACGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATCGAGTCCATGCTCCCGCAGCAACAACTGGGCATCGTTGGT
 GGCTTCATCATCAGATGATTTCAGAAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA
 CGTCTCAAAATTTGCCCCCCGAATCAGCCATCAAAATTCATGGCTTATGAGCAATCAAGCCCT
 TTGTTGGTGAATGACCCAGGAGACTCTGAGGATTCACGAGAGGCTTTGTGGCAGGTCCTTGGCA
 GGGGCCATCGCCAGAGCAGCATCTACCCAATGGAGGTCTTGAGACCCGGATGGCGCTCGG
 GAAGCAGGCGAGTACTCAGGAATGCTGGACTCGGCCAGGAGTATCTGGCCAGAGAGGGGG
 TGGCGCGCTTCTACAAAGGCTATGTCCCAACATGCTGGGCATCATCCCTATCCCGGCATCG
 GACCTTGCAGTCTACGAGCAAGTCTCAAGAAATGCTCAGCACTATGTCAGTGAACAGCGC
 GGACCTCCGGCGTGTGTGCTCTCCGCTGTGGCCAGCATCTCCAGTACTCTGGCCAGCTGG
 CCAGTACCCCTCGCCCTAGTCAGGACCCGGATCGAGGCCAGGCTCTTATTGAGGGCGCT
 CCGGAGGTGACATGAGCAGCCTCTTCAAACATATCTCGGACCCAGGGGGGCTTCGGGCT
 GTACAGGGGGCTGGCCCGCACTTCATGAAGTCACTCCAGCTTGAGCATCAGTACGTTGGT
 TCTACGAGAACCTGAAGATCACCTTGGGCGTGCAGTCTGCGCT**TGAC**CGGGGGAGGGCCGCCG
 GCAGTGGACTCGCTGATCTGGGGCCGAGCTGGGGTGTGCAGGCATCTCAATCTGTGAATG
 TGCCAAACACTAAGCTGTCTCGAGCCAAGCTGTGAAAACCTTAGACGACCCGAGGAGGGT
 GGGGAGAGCTGGCAGGCCAGGGCTTTGTCTGTGACCCAGCAGACCTCTCTTGTGGTCC
 AGCGAAGACACAGGCATCTCTAGGGTCCAGGCTCAGCAGGCTCCGGGCTCACATGTGTAA
 GGACAGGACATTTCTCGAGTGGCTTGCCTAGTGAAGCTTGGAGCCTGGAGGCCGCTTATG
 TCTTCCATTTCACTCTTGCAGCCAGCTGTGGCCACGGCCCTGCCCTGTGCTTCCCTGTGC
 ATCTCCCTGTGCCCTTTGCTGCTGCTGTCTGCTGAGGTAAGGTGGGAGGAGGCTACAG
 CCCACATCCCAACCCCTCGTCCAATCCATAATCCATGATGAAAGGTGAGGTACCTGGCCCT
 CCGAGGCTGACTTTCCCAACTACAGCATTTGACGCCAATTTGGCTGTGAAGGAAGAGGAAG
 GATCTGGCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT
 TGGGAGTGCAGGGGGCTCGGCTGCTTGGCTGCTGCACAGAAGGCCAAGTCTGGGGCTCA
 TGGTCTCTGAGCTGGCTTGGACCTGTGAGGATGGGGCCACCTCAGAAGCAAACTCAGT
 TCCCACTTGTGGCATGAGGCACTGGAGCACCATGTTGAGGGCGAAGGGCAGAGCGTTTGT
 GTTGTCTGGGGAGGGAAGAAAGGTGTTGGAGGCCCTTAATTTATGAGTGTGTTGGGAAGAGGG
 TTTTGTCCAGAAGCAAGCCGGAACAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTCTGACGCCCTGGGGGTTCTGTCCAACC
 CCAGCAGGGCCGACGGCCAGCCCAACATTCACCTTGTGTCACTGCTTGGAACTTATTT
 ATTTTGTATTTTATTGAACAGAGTTATGTCCTAACTATTTTATAGATTTGTTTAAATTAATA
 GCTTGTCAATTTCAAGTTCATTTTATTCAATTTATGTTCAATGTTGATGTGACTTCCCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGGCGCTGCACTGACAT
 CTGTCCAGAGCAAAATCTTTTGGGACTGGAGGCAGAAAGCGGCCAGAGGCAGACGCCCTG
 GCTCCTTTCTTTGGCAGGTTGGGGAAGGGCTTGGCCCCAGCCCTTAGGATTTCAAGGTTTGA
 CTGGGGGCTGGAGAGGAGGAGGAGGAACCTCAATAACCTGAAGGTGGAATCGATTATTTCT
 CTGCGCTGCGAGGGTTTCTTTTATTTCACCTCTTTTCTGAATGTCAAGGCGAGTGAGGTGCCCT
 CACTGTGAATTTGTGTGGGGGGGGCTGGAGGAGGGGTGGGGGCTGGCTCGCTGCCCTCC
 CAGCCTTCTGCTGCCCTGCTTAACAAATGCCGCCCACTGGCGACCTCACGTTGCACTTCC
 ATTCACCAAGAAATGACCTGATGAGGAAATCTCAATAGGATCAAGAGATCAAGAAAAAT
 GTTATATATGAACATAATACTGGAGTCTGCAAAAAGCAAAATTAAGAAAGAAATTTGACGCTTGA
 AAGTGTCTATTAAAGCAGCCTCTTAATAAAGTTGTTTCAAGGTGAAACCACTGTTAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRNGNI
 NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
 GGCTTCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGATCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCTCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGGTTGTGCTGTGCTCTACAATGTACGATCAACAACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGCTCTCTCTTTCTTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAAATAATTCATGTGAACAGTGTGTTAAGAGTGATAAG
 TAAAATGCAGCTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACTT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCTGGAAGTCTATCCCAACATATCCACATCTTATATCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAGGTGCCT
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSESEIKRR
SHLQLLSKASLCVSSFFAISWALLPLSPYMLK

[illegible]

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCGLLYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTTRFPILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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CTTCTGTAGGACAGTCAACAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTCGAAAAGATTCGCAATAAACT
TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
TGAGGCCCTGTGGTCCCCTCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
TTGCTGGTATCACTGCAGTGTCTGTTGCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
CTGTATCAGCTCCTCAGCCAGCTCCTTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCAGCTGTCT
GCTGAAGAACACTTTTCATTTTGAAGCCAGTGTCTGCCAAGGAAAGGAATGCAGCAACACCAG
CGATGCCCTGGACCTTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
AATCTAATGGAACCTTCTGTCTGTGGGAAGCCTGGAAATGCTATGAAGAAGAACAGTGTGTCT
TTTCTAGTTGCAGAACTTAAGAAATGACATTGAGTCTAAGAGTCTCTGTCTGAAAGGCTGTTCT
CAACGTCACTAAGCCACCTGTCACTTCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA
TCTTTTCGAAAGTTTGTAGTGTGCAATGTAAACAGCTTAAACCCACAGTCTGCACCAACCACT
TCCCAACAAGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
GGGACTGCTGCCCTGAGGCTCTGGGGCTGCACCTTGGCCAGCACCCCACTTCTGCTTCTCTG
AGGTCAGAGCAGCCCTGCGGTGCTGCACACCTCTTCTCCCTGCTCTGCCCCGTTTAACTGC
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCAGACGTGCTTCTTCTTCAATTATTA
AAGCACTGGTTTATTCTACTGCCAAAAAATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLET PVR
LYQNMFCSAENCSEETHITAF TVHVS AEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
CPACYESNGTSCRGKPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFE CANVNSLTPTSAPT TSHNVGSKASLYLLALASLLLRGLLP

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCTCACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCC**ATG**GTCCTCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTCTGCTGAATCTGGGTCCCCGGCGGCGGGGGCCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCGAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCTCACCCACAG
 CCATGCCATCTCTGAGGATCTGCGGTGGTCTGATGCCCTGGGGCCCGTGCCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGCACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAELLAATVSTGFSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSP TAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPNRLREECPLDTSLCTDTNCASQSTTSTRTTTTPTPTIHLRSSPSLPPASPCPALA
FWKRVRI GLEDIWNSLSSVFTEMQPIDRNQR

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FIGURE 215

CCCGGGTCGACCCAGCGTCCGGGGAGAAAG**ATG**ATGCCGGCTGGCGGCGGGTTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGGGCTCCAGGGCGACCGTGACCGCGACTGGTACTGCACTGCGAAGAGCA
 GAAGTCTCTGGGGCGCTCTGAATCACTTCCGCTCCCGCAGCCAACTACATGAGTCTAGCAGGCTGGACCT
 GTCGGGACGACTGAAGTATGAGTGTATGTGGGTACCCGTTGGGCTCTACCTCCAGGAAGGTACAAAGTGCCCT
 CAGTTCATGGCAAGTGGCCCTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGCGCGTGGCTCGTTTCT
 CAATGGCTGGCCAGCTGGTGATGCTCTGCCGCTACCGCACTTCGTGGCAGGCTCTCCCCCATGTACACCA
 CCTGTGTGGCCTTCGCTGGGTGTCCTCAATGCATGGTTCGTGTCCACAGTCTTCCACACCGAGGACACTGAC
 CTCACAGAGAAATGGACTACTTCTGTGCCTCCACTGTCATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC
 CGTGGGCTGACGACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACTGGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCTGGTGCCTGTGGAAACAGCGGGCGCTGCCCTACGTGCGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGACGGGGCTGTCCCTGCTCGAGTGTCTGACTTCCACCCGCTCTTCTGGGTCTGGATGCCATGCCA
 TCTGGCACATGACACCATCCCTGTCCAGTCTCTTTTTCAGCTTTCTGGAAGATGACAGCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGAC**TGA**AGACCTTGGAGCGAGTCTGCCCGAGTGGGATCCTGCCCCC
 GCCCTGCTGGCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTCAACTTCTTGAAGTGGACATGA
 AGGATGTGGGCCAGAACTCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCCTTGGAGTCTGTCTAGGG
 AAGGCTCCAGCATCTGGGACTCGAGAGTGGGAGCCCTCTACCTCCTGGAGCTGAAGTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCGTGTTTCTCCCAACAGGCTCTCCCCACATCCCCAGCTG
 CCTGGCTGGTCTGAAGCCCTCTGTCTACCTGGGAGACAGGACCAAGGCTCTAGGGATACAGGGGGTCCC
 CTTCTGTTACACCCCCACCTCTCCAGGACACCACTAGGTGGTGTGGATGCTGTTCTTGGCCAGCCAA
 GGTTCAGCGGATTTCTCCCATGGGATCTTGAAGGACCAAGCTGTGGGATTTGGGAAGGAGTTTCAACCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCTCACATACTCCGTTTTCAGGGCCAGGCTCCAGCAAGCCCAAGGCA
 AGGATCCTGTGCTGTCTGGTGTGAGAGCTGCCACCGTCTGTCCGAGGTGTGGCCAGGCTGAGTGCATAGG
 TGACAGGCGGTGACATGGGCTGGGTGTGTGTGAGCTCAGGCTAGTGTGCCAGTGTGGAGACGGGTGTTGT
 CGGGGAAGAGGTGTGGCTCTCAAGTGTGTGTGTGAGGGGGTGGGTGTGTAGCCTGGGTAGGGGAACGTGTG
 TGCCGCTGCTGGTGGCATGTGAGATGAGTACTGCCGTCAATGTGCCAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCCTGTACCATCAATACTACTGTGAGAGCCAGCTCTGCCAAGAGCCACCTGGCGGACAGC
 CAGGACTCTCCATGCCAGGCTGCCGTGTGCATGTTCCCTGTCTGGTGGCTTTGGCCGCTCTCTGCAAC
 CTCACAGGTCCTCCACAACAGTGGCTCCAGAACAGCCCTCGGAGGCAGAGGAAGGAAATGGGATGGC
 TGGGCTCTCTCCATCTCTTTCTCTCTTGCCTTCGCATGGCTGGCTTCCCTCCAAAACTCCATTCCTCT
 GCTGCCAGCCCTTTGCCATAGCCGTGATTTGGGGAGGAGGAAGGGGCAATTTGAGGAGAAAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTCTTCCCTTCCAGAGGGTCTTACTGTTCAGGGTGGCCCGAGGAGGAGGGGGCC
 AATGAGATGGAGGAGCTCCAGAACTTTCCATCCCAAGGAGCTCCGCTGGTGAAGCAGACTGGATTTTGT
 CTTGCCCTGACCCCTTTCCTCTTTGAGGGAGGGAGCTATGCTAGGACTCCAACCTCAGGAGCTCGGGTG
 GCTTGGCTAGCTCTTTTGTACTGAAACCTTTAAGGTGGGAGGTTGGCAAGGGATGTGCTTAATAAATCAA
 TTCCAAGCTCAAAAAAAAAAAAAA

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FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
 TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFNLGLASLVMLCR
 YRTFVPASSPMYHTCVAFWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
 TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWVLAWCLWNQR
 RLPHVRKCVVVVLLQGLSLELELLDFPPLFWVLDAHAIWHISTIPVHVLFFSFLEDDSLYLL
 KESDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 217

GGCGCGCTGGAATTGTGGGAGTTGTGTCTGCACCTCGGCTGCCGGAGGCCGAAGGTCCTGTA
CTATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
CTGATGGCCGCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCTTGAC
CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAAGAAACCAAGCCGAGGAGGAGC
TGGATGCCGAAGTCTTGAGGTGTTCCACCCAGCATGAGTGGCAGGCCCTTCAGCCAGGG
CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGGCAAA
ACTCCAATATGAGGACAAGTTCCGAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA
ACACCTACACATCTCAGGATCTCAAGAGTGCACCTGGCAAAATTCAGGAGGGGGCAGAGATG
GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCATTTGA
GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTGATTGAGACTGACATGCAGATCATGG
TACGGCTGATCAACAAGTTCAATAGTTCAGCTCCAGTTTGGAAAGAGAAGATGCTGCGCTG
TTTGATCTTGAATATTATGTCACTAGATGGACAATGCGCAGGACCTGCTTTCTTGTGTGG
TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCTCGTGAAGGATATGCTGCGT
TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA
GCCCTGCAAGAGCTGCTGGTCATCTTGGCCACGGAGCAGCCGCTCACTGCAAAAGAAGAAGGT
CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCTTGAAGC
TCGGGGGGCTGCAGGTCCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCCGAGGAGGAGGCTGA
GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
GCCTGTGGGAACAGGGCTGGTGCGAGATCAGGGCCCACTCCTGGCGCTGCCGAGCATGAT
GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCCTACCG
TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
GCCTGGAGCTGCAGGATGGTGAGGACAGGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
AGCTTGCTGAAGGAGCTGAGATGAGGAGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
GGCTGAGGGGTGCCACGCTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT
TGGCCATTTAAATGGAACCTGAAGGCCAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEDEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSSLRHFFYAQRQFLKL
 GGLQVLRTLVQEKGTEVLAVRVVTLTYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

TTTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCCCTTCCC
CTTCCCCGGGGTTCTGGGGTGACATTCACGCCGCCCTCTGGTGGGTTCGGTTGCCACCCCA
CGCGGACTCCCAAGTGGCGGCGCCCTCCCATTTGGCTGCTCTGGTACGGGCCCAACCCCA
TTCCACACCTTGACACGCCATGGGGGGCTCGGGTGTTTTTTCGGCTGCACTTTCGTTCGGCTTCGCG
CCGGCCCTTCGCGCTTTTCTTGATCAGTGTGGCTGGGGAGCCCGCTTCGGTTTCATCTCTGGT
CGCAGGGGACATTTTCTGGCTGGCTTCCCTGCTCTGGCCCTGTGGTCTGGTTCACTCTGG
TCCATTGTAGCCAGCGCTCAGATGCCCGGCTCCAGTACGGCCCTCTGATTTTGGTGTCTGG
GTCTCTGTCTTCTACAGGAGGTGTCCGCTTTGGCTACTACAAGCTGCTTAAGAAGGCAGA
TGAAGGGTTAGCATCTCGTGTAGTGAGAGCGGAAGATCACCCATCTCCATCCGCGACCATGGCC
ATGTTTCTGGTCTCTCTCTCGGTATCATCATGTGTGTCTTCTCTGTATTCAATATTTGGCT
GATGACTTGTGGCCAGGTGTGGTGGGATCCAGTACGAGACTACCCATTACCTTCTGACTTC
AGCCTTTCTGACAGCAGCCATTATCTGTCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
CGGTGTGAGAGGACGAGCTATGGGCTTTGGGCCCTGGTGGTGGGAGTACCTACTGACATCTG
CCACTGACATTTCTGAACCCCTGGTATGAGGCCACGCTGCTGGCCATCTAGTCAGTCACTGT
TTCCATGGGGCTCTGGGCCTTCTGACACAGCTGGAGGGTCCCTCCGAAGTATTACGCGCAGCC
TCTTGTGTAAAGGACTGACTACCTGGACTGATCCGCTGACAGTCCCACTGCCCTGTCCACT
CCATGACTGAGCCAGCCCAAGCCCGGGTCCATTGCCACATTTCTGTCTCTCTCTGTCTG
GGTCTACCCCACTACCTTCTCAGGGTTTGTCTTGTGCTTTGTGACCGTGTAGTCTTAAGTCT
TACCAGGACGAGCTGGGTTCAGCCAGTCACTGATGCTGGTGGTTGAATCTGCATCTATCCC
CACCACCTGGGGACCCCCCTGTGTGTCTCAGGACTCCGCCCTGTGTCACTGCTCTGCTCTCAC
CGTGCCAAAGACTACCTCCCTTCCCCCTCTCGAGCCGACCGCAGGAGGAGCTGGGTGAT
GGTGATTTCTGCCCTGCGCATCCCAACCGAGACTGAGGAACCTAGGGGGACCCCTGGGC
GTGGGGTGCCCTCTGATGTCTCGCCCTGTATTTCTCCATCTCGAATTTCTGGACAGTGCAG
CTTGGCCAAAGGAAGGACCTAGTTTATGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTC
AGGCTGAGGGGGGAACATTTTGGTGTGATGATAAATACCTAAATCGGCTTTTCTCTTTT
GAGTGGGGGGAGGAGGAGGATATTTGAATCTTCTAACCTCTTGGCTTATTTTCTCTC
TCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCCGTCCTTTCTCCTTGGTCCCAGACCTT
GGGGGAGGAAGGAAGTGCATGTTTGGGAAGCTGGCATTTAGGGAACAAATGGTTTAAACCT
CCTTAACCAACAGCATCTCTCTCTCCCAAGGTGAAGTGGAGGGTCTGCTGTGGTAGCTGGC
CATCCAGAGCTCGAGTGCACCTGGAGGATTCAGACTACCATACCATCTGATGGGAAGGAGGG
GAGATTTTGTAGTTTAAATTTGGGGTGTGGGAGGGCGGGGAGCTTTTCTATAAAGTGT
ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCTTTAACTCAAGGTGATTGTGATTTTGAAT
ATAAAAAAAGAAATTTGTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAPALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIIHGDSPIYFLLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCKD

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AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTCTGTTGAGTGAGGACGGAAGATCAACCCA
 TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
 TCACCCATTANTTCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTATAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCTTTCCCTTTCCCCG
GGGTCTGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTGCC
TTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATTCAATATTTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTGCGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGTCGCAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTGGCTGATGCACIT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGCAGGGAAGGAGAGG
 TGTCGTGTGCGTCTCGACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTGCGCAACAATGATGTTTCTGTGACCAACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGGTGGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCCTGTCAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCTGGCTACTCCACCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTCGTCCCCTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGAGATTACCCTTGTCGCCGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TGA**ATCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCCATTGGGCTGACCGTGTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAACGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTTAT
 CCTCAAGCTCAGGGCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA
 CTGAGAAGTGAAAAA

FIGURE 226

MATARPPMMWVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCPsAGTKCL
VSGWGTTKSPQVHFVKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDS CQGDSSGGP
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCCGCGCGA
 CAAGCGCGAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGTCTGCTGGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTCAACGGTGCCGTGCTCTTCTGAACCAAGCCACGCGCCGCGGACAG
 GCGGCCCCACCTTCTGCTCAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGTGTCTGTGGA
 AAGGGCGGACAGCTGCGACCTCAGCATCTCTATTGACCCGCGCTGCCCGACCTCAGGCACA
 GCTTCCGACCGCTGGAGAGCGCCAGGCTCCGTGCTGCAGGCGCTGACAGAGCAACAGGCGC
 CAGCCACGCTGTGTGGCCAGGACGAGCAGGAGTGTGTGACACGCTGGCCGACAGCTGCC
 CCGGCTGTGGCCGAGCCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGGCGAAGGGGATG
 GCACGCTGGGCGAGGGCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCTCATCCAGCTTCTC
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTACGCGACATCTGGATGCCCT
 GCAGAGGGACCGGGGGCTGGGCGGCGCCGCAACAAGGCCGACCTCAGAGAGCGGCTGCC
 GGGGAACCGGGCCCCGGGGCTGTGCCACTGGCTCCCGGGCCCCGAGACTGTCTGGAGCTCTC
 CTAAGCGGACAGCAGGACGATGGCGTCTACTGTCTTTCCACCCACTACCCGGCCGGCTT
 CCAGTGTACTGTGACATGCGCAGCGGACGGCGGGCTGGACGCTGTTTACGCGCGGGGAGG
 ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACGCGTACCAGAGACGGCTTGGCAGGCTCACC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCT
 GCACGTGGACCTGGAGACTTTGGAATGGACGCCCTATGCCCGCTACGGGAGCTTCGGCG
 TGGCGTTGTTCTCCGTGGACCTTGAAGAGACGGGTACCCGCTCACCGTGGCTGACTATTCC
 GGCACTGCAGGCGACTCCCTCTGAAGCACAGCGGATGAGGTTACACCAAGGACCGTGA
 CAGCGACCATCAGAGAACAACTGTGCCGCTTCTACCGCGGTGCCTGGTGTACCGCAACT
 GCCACAGCTTCAACCTCAATGGGCACTACCTGCGCGGTGCGGAGCGCTTGTGAGATGAAGATCCG
 GTGGAGTGGTCTCTTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 CGGGTCCGGGAGGACCG**TAG**ACTGGTGCACCTTGTCTTGGCCCTTGGTCCCTGTGCGC
 CCCATCCCCGACCCCACTCACTCTTTCGTGAATGTTCTCCACCCACTGTGCCTGGCGGAC
 CCACTCTCCAGTAGTGGGAGGGGCGGGGCCATCCCTGACACGAAGCTCCCTGGGCGGGTGAAGT
 CACACATGCCCTTCTGCCGTCCCACCCCCCTCCATTGGCAGCTCACTGATCTCTTGGCTC
 TGCTGATGGGGGTGCGAACTTGACGACCCCAACTCTGCTGCCCTGCCCCACTGTGACTCCGG
 TGCTGTTTGGCGTCCCCTGCCAGGATGGTGGAGTCTGCCCCAGGCAACCTTGCCTTGGCC
 GGCAATAATCCGGCAATTATGGGACAGAGAGCAGGGGGCAGACAGCCACTTGGATGCCCTC
 CTAGCAGATCGTGGGGAATGTGAGGTCTCTCTGAGGTGAGTCTGAGGCCAGTATCTCTCCAG
 CCTCCCAATGCCAACCCCAACCCGTTTCCCTGGTGCCAGAGAACCCAGCTTCCCCCAA
 GGGCTCAGCCTGGCTGTGGGCTGGGTGGCCCATCTACAGGCCCTGAGGTCAAGATGGG
 GAGCTGTCTGCTTTGGGGACCCACGCTCCAAGGTGAGACCAAGTTCCCTGGAGGCCACCCAC
 CCTGTGCCCGGCGAGGCTGGGGTCTGCAGTCTCTTACCTGTGTGCCCACTGTCTCTGT
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGCTCCCGGCCGCTCCTTACCTGGGGCAGC
 CGGGGCTGCCATCCCATTTCTCTGCTCTGGAAGGTGGGTGGGGCTGCCACCTGGGGCT
 GGACTGCGCTAATGGGAAGCTCTTGGTTTCTGGGCTGGGGCTAGGCAGGGCTGGGATGAG
 GCTTGTACAAACCCCAACCAATTTCCAGGGACTCCAGGGTCTGAGGCCCTCCAGGAGG
 GCTTACAGGGGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCTTGGC
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCCCGGCGAGTGTCAAGGGACAGGGA
 GGTGCTACCCGGCAATGGGGTTCGGGGGACTCGGGGCAACAGCAGCCAGCCACCTGGACA
 CTTTCTTGTGTAATCTCCCAACACCCAGCAGCTGTATCCCACTCCTTGTGTGCACACA
 TGCAGAGGTGAGACCCGAGCCTCCAGGACAGCAGCAGCAGGCGAGGGCTGGAGCGGG
 TCTCAGCTGTCTGTGTCAGCAGCCTGGACCCGCGTGGCTTACGTCAAGGCCAGATGACAGG
 CGGCTTCCCAAGGCCCTCTGTATGGGGGCTCCGAAAGGCTGGAGTCAAGCTTGGGGGCT
 GCCTAGCAGCCTCTCTCGGGCAGGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA
 GTTGCTCAGGGGTGTGGGGTTCGGTTCTCCCTTCCCTCCCACTGAAGTTTGTGCTTAAAA
 AACATAAATTTGACTTGGCACCACTGGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTC
 TGTCCAGTGCCACAGGTGATCCACATGCGCAG

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MNVDRWKTMGAAQLDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
 APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
 QPRLVGDQDQELDLTADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
 SESQGHMAHLVNSVSDILDALQDRDLGRPRNKADLQRAPAGTRPRGCATGSRSPRDCLDVL
 LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTFVQRRDGSVNFRRGWDAYRDGFGRLT
 GEHWLGLKRIHALTTQAAELHVDLEDFENGATAYARYGSFGVGLFSVDPEEDGYPLTVADYS
 GTAGDSLKHQSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLNGQLYRGHAHSYADG
 VEWSSWTLGWYSRLKSEMKEIRFVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCCCTGAAGTACAGTACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGTCTGAGCTGTATAACAAGCTGGAGCACAGGTGCAGCCCTTGTACAG
 AACAAATGAAATGGCATGGAGACAATTGTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAATATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAAACAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAATAGCAGAGTGAGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCATAATGTATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCTTACACTTGGTGGAAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAATACACAAGGAATTCTTTTTGTTGTTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTACATTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCCATTAAGACTCTGATAATTG
 TCTCCCCCTCATAGGAATTTCTCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAA

FIGURE 230

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPPSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGECD

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PAGE 230/330

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTNTGCAGCAT
GTGGCTGAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

FIGURE 232

GCGGAGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTCCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGTCGCCGCCCTCTCGAGATCTCTGGCTGCT
 CTGGGGTTTCGCGGGGCGCGGGGACCCGCGGTCCGGGCGCGC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGCGCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGGTCTACCCCTGAGCCT
 GCTCAGCGTCACTGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCAACCTGGAGACTCTG
 AGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCGGCCCAACTCGGTGACGCCCCGAGCG
 GAGCGCAGAAGCCCGGGGCCGCGCAAGGCGCGGGGAGAATTGGGAGCCGCGCTCTTGCC
 CTACCACCCTGCACAGCCGCGCCAGGCGGCCAAAAAGGCCGTGAGGCCCGCTACATCAGCA
 CGGAGCTGGGCATCAGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCCGACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCACGGGGCGCGCGGGCCCACTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACACTTTGAC
 TGGTTCTTCTGGTGCCTGACACCACCTACACCGAGGCGCACGGCCTGGCAGCCCTAACTGG
 CCACCTCAGCCTGGCCCTCCGCGGCCACCTGTACCTGGGCGCGGCCAGGACTTCATCGCG
 GAGAGCCCAACCCCGCGCTACTGCCACGGAGGCTTTGGGGTGTCTGCTGCGCGCATGCTG
 TCGAAACACTCGGCCCACTGGAAGGCTGCCCAACGACATGCTAGTGCGCGCCCTGA
 CGAGTGGCTGGGTGCTGCTGATCTCGATGCCACCGGGGTGGGCTGCATGGTGACACGAGG
 GGGTGCACTATGACCTCTGAGCTGAGCCCTGGGAGCCAGTGCAAGGAGGGGCCCTCAT
 TTTCCGAAGTGCCCTGACGCCCAACCTGTGCGTGACCTGTGCACATGTACCAGCTGCACAA
 AGCTTTGCGCCGAGCTGAACCTGGAACGACGCTACCAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACCGCACTCTGGCCGTGATGGGGACCGGGCAGCTGTGGCCGCTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCTGCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACCACCCGGCCCTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGA
 ATACAGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGAGGCCGCGCGGCCCTCACTC
 GCCGAGTGCACTGCTCCGCGCGCTGAGCCGCTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCCCTCAGCTCTCACTGTGCTGCTGCTCTAGCTCGGGCTGAGCGTGACCTGGCCCTTG
 CTCTTTGGAGGCCCTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGCGAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGGCCATCGAGATGTCTTCGACCT
 GTCAAGGCCACGTGGCAGAGCTGGAGCGCGCTTTCCCGGTGCCCGGGTGCCATGGCTCAG
 TGTGCAGACAGCCGACCTCACCCTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGC
 TGGACACACTGTTCTGCTGGCCGGGCCAGACACGGTGCTCAGCGCTGACTTCTGTAACCGC
 TGCCCATGATGCCATCTCGGGCTGGCAGGCCCTTTTCCCATGCACTTCCAAGCCTTCCA
 CCCAGGTGTGCCCCACCACAAGGGCCTGGGCCCCAGAGCTGGGCCGTGACACTGGCCGT
 TTGATCGCCAGGCAGCCAGCGAGGCTGCTTCAACTCCGACTACGTGGCAGCCGCTGGG
 CGCCTGGCGCAGCCTCAGAACAAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAAGCCT
 ACCGGGCCAGACGTGACGCGCAGGCTCAGTGAGGACCTGTACCACCGCTGCCCTCAGAGC
 GTGCTTGAAGGCGCTCGGCTCCCGAACCCAGCTGGCCATGCTACTTTTGAACAGGAGCAGGG
 CAACAGCAGC**TGA**CCCCACCTGTCCCCGTGGCCGTGGCATGGCCACACCCACCCCACTT
 CTCGCCAAAACAGAGCCACCTGCCAGCCTGCTGGGCAAGGGCTGGCCGTAGCCAGACCCC
 AAGCTGCCCACTGTGCCCTCTCTGGCTCTGTTGGTCCCTGGGCTCTGGACAGCACTGGG
 GGACGTGCCCCAGAGCCACCCACTTCTCATCCAAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTTCGGGCTGTGGCCCTCCACGTATTATGAGCTACAGTCTGCCCTGACGCCACGCCCTGC
 CTTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAAGGAGGAGCTGAGAGGGGG
 GCATCTCCCAACTTCTCCCTTTTGGACCCCTGCCGAAGCTCCTTGCCCTTAATAAACTGGCCA
 AGTGTGGAAAAA

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FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELP PRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKKAVRTRYISTELGIRQLLVAVL
TSQTTLPTLGVAVNR TLGHR LERVVFLTGARGRRAPPGMVVTLGEERP IGH LHLALRHLL E
QHGD DFDWFFLVPD TTYTEAHGLARLTGHLSLASAAHLYLGR PQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPD EWLGR CILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALT AHPVRDPVHMYQLHKAFARAELE RTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADV LGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAAL TLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTL FLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHFGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLR AVEPALLQRYRAQTC SARLSEDL
YHRCIQSVLEGLGSRTQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTGGCGAGGGCCCGCTTTTAGAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCAACCGATTTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCTT
 TTCCCCGCCCCTGAGACCCCTGCAGACCATCTGT**CATG**CGGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGCTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCCGCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

Region	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)
Asia	1980	3.1	1.1	35	150	1,100
Latin America	1980	2.1	1.1	52	150	1,100
Europe	1980	0.7	0.6	86	250	2,200
North America	1980	0.3	0.2	67	250	2,200
Africa	1980	0.4	0.1	25	50	400
Oceania	1980	0.03	0.02	67	10	100
World	1980	4.6	1.8	39	100	700

Region	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)
Asia	1980	2,250	600	27	150	1,200
Latin America	1980	350	150	43	100	1,500
Europe	1980	550	450	82	250	2,500
North America	1980	250	200	80	300	3,000
Africa	1980	350	50	14	50	500
Oceania	1980	30	10	33	10	1,000
World	1980	4,700	1,400	30	150	1,200

[illegible]

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCGCGCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCAGCA
AGATCCAG

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FIGURE 237

GCGGCGGGCT**ATG**CCGCTTGCTCTGCTCGTCTGTTGCTCTGGGGCCCGGGCTGGTGCCT
 TGCAGAACCCCCACGGCAGAGCCTGCGGGAGGAACCTTGTCATACCCCCGCTGCCCTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGCACGCGCTGGGATTCCGAGCTTCAGCGGGAAGGAGTG
 TCCCATTTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCACTTACACAAGGCTTTTGGAGGACCCGATATCGGGGCCACCCTTCTGTC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTTCGCGCTCTCTCAACTCATPCGA
 CTCACCAACACAGTCACTCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCGAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACCAAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAAGTTGATTTGATGCCTTC
 ATCAGGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCGAACCCCTCAGGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATACCACTACAACCAAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCATCCTAGGCAT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGGGAAGAGACCCCAAGAGATGAGGCCCCCTCAGTGCCCTTCTGTC
 ATGCCACGGGTACGTGATGGCTATGGGTGCAGAAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGGCTTCCCGGTGCTGCTGCTGACACCGTACCTTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTAGCTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTCAGCCATCTGTCTCAGCGCCCTTGTCGCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCAGTGCCTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTTGGCCAAGCGGCTGGCCAACTTATCCGGCGCGCCGAGGTGTCCTCCCACTCTGAATT
 CTTGCCCTTTCACGACGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAGTGCCTTGGACCAGGTCAAGGC
 CTACAGCTGTGTTGTCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAAATTGAATTAA
 CTTAGAAATTCATTTCTCACCTGTAGTGGCCACCTCTATATTGGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGATTGGACAGCACAGAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTTGTGGAATAAAAAACGGCTGTTTCCGTGGAAAAA

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FIGURE 238

MPLALLVLLLLGPGGWCLAEFPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDSWK
ELSNVLSGIFCASLNFIDSTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCARNARCTSSISWELRQTLSSVVFDAFITG
QGKKDWSLFRMFSTRLTTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT
YAIYDLDDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWPYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLNLPTPDFSMPYNVICLTCTVAVCYGSFYNNLLTRTFHIEEPRTGGLA
KRLANLIARRAGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGGAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGAATGCTGGGTCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTCCCCAAAAGAGGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAACTGTAAAGAAATAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 242

MRSLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGAVSTRTRQKGVTTAVIPPEKKPQATPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF
 NQSEWDRLEHFAPPPFGFMELNYSLVQKVVTFRPPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFL
 RYMKNRFLRSKTLDDGAHWRIYRPTTGALLLLTALQCDQVSAYGFTIEGHERFSDHYDTSW
 KRLIIFYINHDFKLEREVWKRHLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGTCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAACACTTCCATAGACTTTATCACACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

FIGURE 244

MRGPGHPLLLGLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

The figure shows a vertical sequence of chemical structures illustrating the proposed mechanism for the formation of the $[Cp^*_2Ir(\eta^5-C_5H_5)]^+$ cation from $[Cp^*_2IrCl_2]$. The steps are as follows:

- $[Cp^*_2IrCl_2]$: A square planar complex with two Cp^* ligands and two trans-chlorine atoms.
- $[Cp^*_2IrCl] + Cl^-$: An intermediate where one chlorine atom has been removed, leaving a vacant site.
- $[Cp^*_2Ir] + Cl^-$: A further dechlorination step, resulting in a complex with a vacant site and a terminal hydride ligand (H^-).
- $[Cp^*_2Ir(H)] + Cl^-$: A complex with a terminal hydride ligand and a vacant site.
- $[Cp^*_2Ir(H)Cl] + Cl^-$: A complex with both a terminal hydride and a terminal chlorine ligand, and a vacant site.
- $[Cp^*_2Ir(H)(\eta^5-C_5H_5)] + Cl^-$: Coordination of cyclopentadiene to the vacant site, forming a η^5 -cyclopentadienyl complex.
- $[Cp^*_2Ir(H)(\eta^5-C_5H_5)] + Cl^-$: Further coordination or rearrangement leading to a more stable η^5 -cyclopentadienyl complex.
- $[Cp^*_2Ir(\eta^5-C_5H_5)]^+$: The final product, a cationic complex with two Cp^* ligands and one η^5 -cyclopentadienyl ligand.

FIGURE 245

GGGCTGGGCCCCGCCGACGTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCTGGTGCTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTGTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGTAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAAACAGGAGCTGAACTAGA
 ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTGTCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAGCTGTAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRGSWHPGFNCEFFTFCGGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPSPGPAPQYPLYPAGPPVYNPAAPPP
YMPQPSPYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

GGGGAGCTAGTGGCGGGGCGCAGTGGTGGTGGGGCGGCGCAAGGGTGAAGGGGGCCCCAGAA
 CCCCAGGTAGGTAGGACGAAGAGATGGCGTGTTTGTGCCCTCAAAATGTCCTTGCACCACTG
 TCATTTCATTCTTCCTCACTGTGGCTCTCTTAAGTGTGTCACTCCTCATGGTGTACAGAG
 CTCAGGAAGCATCTCCAAAAGCTAGTGTAGGACGACCAATTCCTTGGAAATAAAATACGACTTC
 CTAGTAGCTCATCCGAGCTTCATTATGATCTCTGTATCATCATGCAAACTTACACGCTGACC
 TCTCTGGGGAACCAACGAAGTAGAAATACACGCGAGCTCAGCCGACCCAGCATCATCTGCA
 TAGTCAACCACTTCGAGATATCTAGGCGACCTTCAGGAAGGGAGCTGGAGAGGGCTCAGG
 AAGAACCTCTGCAAGTCTCGGAACACCCCTCTCAGGAGCAAAATGTCATGCTGGCTCCCGAG
 CCCCCTCTGTGGGCTCCCGTACACAGTTGTCTATCTACATGCTGGCAATCTCTGGAGA
 TTTCCACGGATTTTCAAAAAGCACTTACGAACCAAGGAAGGGGAATGAGGATCTACGAC
 CAACCAAAATTTGAACCACCTCGAGCTAGAAATGGCTTTCCCTGGTTTGAATGAACCTGCTCT
 AAAGCAAGTTTCTCAATCAAAATTTAGAAGAGAGCCAGGCGACCTAGGCATCTCTAATATCT
 ATTTGGTGAATCTGTGACTGTGTGTGAAGGACCTATAGAAGACCTTTTGATGTCACTGTGA
 AGATGGAGCACTTATCTGGTGGCTCTCATCAITTCAGATTTTGAGTCTGTGACAGAGATAAAC
 AAGATGGAGTCAAGGTTTCTGTATGTGTGCGCAGACAGAAGATAAATCAGCAGAGATTGCG
 ACTGGAGTCTCGGGTGACTCTTCTAGAAATTTTATGAGGATTTTCTAGCATACCTGATATCCC
 TACCCAAACAGATCTTCTGCTGGCTCCGAGTTTCTTATGTTGTGTGCTATGGAATCTGGGA
 CTGACACCAATATAGAGAAATCTGCTCTGTGTGTTGATGTCAGAAAAGTTCTCTGCATCAAGTAA
 GCTTGGCATCACAGTCACTGTGGCCATGAAGTGGCCCACTGAGTTTGGGAAGCACTGGTGT
 CTATCGAATGGTGGAAATCTTCTGGCTGAATGAAGGATTTGGTGAATTTGGGAGTGTGTG
 TCTGTCAAGTGGCAATCTCTGAAATCAAGAGTGAAGATTTCTTTTGGCAAAATTTTGA
 CGCAATCAGGTAGACTCTTCTTAAATCTACAGATTTCTATGCTAAGCAGCTGTGAATCTGCTG
 CTAGATCACTGGGTTCTGTTGATGATGTTTCTATGCTAAGCAGCTGTGATTTCTGAATATG
 CTAAGTACAGTCTCTAGCCTGACCACTTTAAAGCTGTATTTGTCACAGTATCTCCAGAGCA
 TCTAGATAAAATACAGAAATGAAACCTCTGGGATATTTGTCACAGATTTTGGCTACAG
 ATGCTGTAAAGGATGAAATGCTTTTGGCTAGAGATCAACATCTATCTCATCTCACAT
 TGGCATCAGGAAGGGGTGGATGTGAAACATGATGAACATTTGGACATGCAAGGGGGTTT
 TCCCCTAATAACCATCACAGTGAAGGGGAGGAATTACACATGAAGCAAGCACATCATATGA
 AGGGCTCTGACGGCGCCCGGACATGGGTACCTGTGGCATGTCCATGTACATCTACAC
 AGCAAACTCAACATGTCCTCATGATTTTGTCTAAAAACAAAACAGATGTGCTCATCTCCC
 AGAAGAGGTGGAATGCAATCAAAATTAATGTGGGCATGAATGGCTATTACATTTGTGCATTACG
 AGAGTATGGATGGGACTTTTACTTGGCTTTTAAAAGGAACACACACAGCATCAGCATC
 AATGATCGGGCAAGTCTATTACAATGCATTTCACTGTGCTAGCTTTGGGAAGCTGTGCAT
 TGAAGAAGCCTTGATTTTATCCCTGTACTTTGAACACATAAAATGAAATATGCCCGTGTTC
 AAGTTTGAATGACTGATTCCTATTGTATAGTTTAATGGAGAAAGAGATATGAATGAAGT
 GAAATCAATTCAAGGCTTCTCATCAGGCTGCTAAGGGACTCATGTATAAGCAGACATG
 GACAGACAGAGGGCTCAGTCTCAGACGAAATCTCGGGAGTGAATCACTACTCTCCGCTGT
 TGCACAACTCATCAGCGTGTGCTACAGAGGGCAGAAGCTATTTCAGAAAGTGGGAAGGAATCC
 AATGGAAACTTGAGCTGCCCTGCTGACAGCTGACCTTGGCAGTTTGTGCTGTGGGGGCCAGAG
 CACAGAAAGCTGGGATTTCTTTATAGTAAATATCAGTTTCTTCTGCTAGTATGAGAAATCT
 GAAAATTTGAATTTGCCCTCTGCGACGACCAAAATTAAGAAAGCTTCAATGGCTCATAGAT
 GCAAGCTTTAAGGAGATAAAATAAAAACTCAGAGATTTTCCACAAATTTTACACTCATTTGG
 CAGGAACCCAGTAGGATACCCACTGGCTGGCAATTTCTGAGAAAAAATGGAACAAACCTGT
 TACAAAAGTTTGAATTTGGCTCATCTTCCATAGCCCACTGGTATGGGTACACAAATCAA
 TTTCTCCACAGCAACCGGCTTGAAGAGGTAAAAAGATTCTCAGCTCTTTGAAAGAAATATGG
 TTCTCAGCTCCGTTGTGTCTCAACAGACAAATGAAACCATTTGAAGAAACATCGTTTGGATGG
 TATAAGAAATTTGATAAAATCAGAGTGTGGCTGCAAAAGTAAAAAGCTTGAACGTATGTAAAA
 TTTCTCCCTTGTCCGGTTTCTGTATCTCTTAATCAACCAACTTTTGTGTAGTGTATTTTCAA
 ACTAGAGATGGCTTGTTTTGGTCCAACTGAGATATCACTTTTTCCTCTCAACTCATTTTGTGA
 TCTCCCTGTGAAAAGAAATAGCTGTAGTTTTCATGATGGGCTTTTTCATGATGGGCTGA
 TCGCTACCAATGTGTTTGTCTCATCAGGTTGTGGCTTGCACAGGATAAACCAAGTGTGGGT
 TCCCTGCCACGAGGAATAAAGTACCTTATTTCTCTCAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFFWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSYILVA
 FIIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWNNDL
 WLNEGFAKFMFVSVSVTHPELVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGMDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGHTTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKMRDMNEVETQFKAFLIRLLRLDIDKQTTWTDGGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC
 RTQNKELQLWLLDESFGDKIKTQEFQILTLIGRNPVGYPYPLAWQFLRKNWNKLVQKFELGS
 SSIAHVMVGTNTQFSTRTRLEEVKGFSSSLKENGSQLRCVQQTETIETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCTAGAGCGCGGTATTACTGCTGGCCCTCTGGGGTTATCCTCCCA
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTAGCCTGGTGCTCTCCAAGGGTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGAT
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAGATTGGGCCCTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTCCTGACCTGTCACTGGGGGACCACTTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
GTGTCAGCACTGTTGGGGCTCAAATTCAGAGAAGACCACCATCCACTCAGCCCCCTCTGGG
GTGCTTGTGGCCTCCTATACCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTCAGGGCTGCGTGGCCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGTTTGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTTC
ACATCTGCTCCATGAATCACTTCCCCACACACAATCATTATATCTACTACCTAACAGCA
CAACTGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGATGTATCTGATAATACAGACGCTGTCCTTTCA

FIGURE 250

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLRLRGGGIFSNLRVQGCMPPQGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC
PSC

[illegible]

FIGURE 252

MRGNLALVGVLI SLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSGDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGTCTTAGCCAGTTCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCAGAAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCTGGGAACAGAGGAGCAGAGACC
 TTTATAAGACTCTCTTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCAATCCCCAGGTGCGCAGCTCCTGTTACCTTTCTCTTCCTGTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTACCTGACCCTGGTGTGGAAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTAGAGTTCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTATTCCTCAACAATAAAGGATTTTGCATATGAA
 AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLQQLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGTTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGACTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCTGGTGGTGTGCATCCCCTTGGGGC
 TGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACAAAGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAAGCGCGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTTGTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTACGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAACCTCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTACCCCTGTCTGGCTCTGGCTCTGTTCTTAAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACCTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGAGAGTCTTCCCTCGCGTGGTGGCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACC CGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAACCTTCCTCTCTGGCTGGTTTTCCAGAACTACAGAGGAATGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGCCATCCGTGACGTATGAATGGCTT
 TTTAAACAAACCCAGTCCCAGCCTGGGTAACATGGTAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCACACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCAAAA

256/330

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLVFCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

AAGGAGAGGCCACCGGGACTTCAGTGTCTCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCTTGTCTCTCTTGAACCTCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCTCTTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAGCTCTGCCTCTCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATTGCAAGATCTCAACCACTGGTGTCTGCAACACAT**GCA**AGCCATTGAAGCCTG
TGCTCTCTTGGCGCCGGGCTTTTGGCCGTTGGTGCAGGAGGACGGCCGACCCCTGCTTT
CAGCAGGCCCCACCCCTCTGAGTGCGCAATAAAATAAAATTCGGTATGCTG

FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAACGTTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCTCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCTATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

0909/27.4.1994

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGG**ATG**ATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCTTGCAGCTTTCTGCCCCCGCCGAGCTGTAC
 CCAGAGCCCGCATGGTGCACTTACATCTACAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCCCAAGCAACGAGGGCATACATTCAGAAGATTCCAAGAGTTCTCAAAAAATATA
 TCTGTCACTGCTGGGAAGATCTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCCTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAGATGCTGTCTATA
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGTGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCCATAGCCATTGGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTATGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCCAAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTTACAACCTCCAGACAAAGAGAAA
 GCTGCCCTCTGAAG**TAA**TGCAATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTC
 TACAGGACAGTGAAGGCTATAGCCCCCTTCAACAATATAGTATCCCTCTAATCACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCTGGCTCTCAAGGATACCCACATTTCTGATCAGCCCTACTTCAAGCCTTTTGTGTTTACT
 GCTCCCCAGCATTTACTGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCCTAATATTCCACCCTGGCTTTTCTCTCCCCTGGCCCTTGTGTAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATAATTCTCCCATTTTCACTGCCCAACTAAAAATACTATTAAATATTCTTT
 CTTTTCTTTTCTTTTTTTTGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTCC
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAAATTAACATTGTAATATCGCTTT
 CCAGGTGTGGAGTGGTTGACATCATTTGAATTTCTCGTTTCACCTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCACTGATAGTTTAGGTGAGTAACACAATTAACAAGTGAAAGATACAGC
 TAGAAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTTTCAGCCATAAAAAATAAGTCTGTCCC
 TTTAGCCAGTTTTTCATGCTGCACAAGACCTTTCAATAGGCCCTTTCAAATGATAAATCCTCC
 AGAAAACCAAGTCTAAGGGTGAGGACCCCAACTTAGCCTCCTCTTGTCTGTCTGTCTGTCTGT
 TTCTCTCTTTCTGCTTTAAATTTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAFLPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL
QEAEEEKKIRTLNLNASCNDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWSQGTGQVIYKGFLEFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNFFPKRPRSHSMIH
YNPRDKQLYAWNENQIIYKLQTKRKLPLK

0939727.11901

FIGURE 263

GGGCGCCCGCTACTACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTGCGAGCTCATGGGGCTGTCGGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGAGGAGAGGAGCGGCCGGCCCGCTGCCAAAAAGC
 AAATGGATTTCCACCTGCACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTTC
 GGAAGGAGAAGCCTCAACAACACAACCTTACCACACCGCCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACCAGCA
 TGAGAGCCAACGTGGAGCTGGACCACGCCACCTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAAACGGGGACACCCCTCCGTGCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTCACAGCCACCCCAGAGGACTTCCCTAAAAAGCACAAGGCGCCTGTCA
 TCGACATTGGCATTGTCAACAGGGGAAGTTATCATGACTGCCTCCAGTGACACCACTGTCT
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAAGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAA
 CTAAGAGGGCCACTCCGCGGCTGTGCACCTCGTTTGCTTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGAAACTGTGGGACACAGATGTGGAATACAAGAAGAGC
 AGGACCCCTACTTGTCTGAAGACAGGCCGCTTTGAAGAGCGGGGGTCCGCGCCGTGCCGC
 CTGGCCCTCTCCCCAACGCCAGGCTCTTGGCCTTGGCCAGTGGCAGTAGTATTATCTCTA
 CAATACCCGCGGGGCGAGAAAGGAGGAGTGCTTTGAGCGGGTCCATGGCAGTGATTCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCCTCTGTGGGACCGGGCGGTGCGGCTG
 TTTCAACACATCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCACAGAGACACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCTTGA
 AGAGCCTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCGGCCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCAGCTGCTGCCATCTTTCCTCCAGGTGGAAGCCTTTCAGAAGG
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCATTGAAACTACTCTTGCTACTT
 AGGTCTCTCTCTTCTTGTGCTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTC
 CTCCCAGGCCAGTGGGTGGAATCTGTCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTTTGGCCCTGTGGCAGCACATCCTCACACCCAAAGAAG
 TTTGTAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTCAGGA
 TGGGAGACTGGGATAGCTTCCCATCACAGAAGCTGTGTTCCATCAAAAAGACACTAAGGGATT
 TCCTTCTGGGCCCTCAGTTCTATTTGTAAAGATGGAGAATAATCCTCTCTGTGAACCTCTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAAGTAGAAAAAGAT
 AGTACTATTGTCCAATGTCATGAAAGTGGTAAAAGTGGGAACCAAGTGCTCTTGAACCAAA
 TTAGAACACATTCCTTGGGAAGGCAAGTTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTGGGAGATGATATCTTGTTTAAGGAGACCTCTTTCAGTTTCATCAAG
 TTCATCAGATATTTGAGTGCCCACTCTGTGCCAAATAAATATGAGCTGGGGATTAATAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRITRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPCRAFIVWLANGDTLRVFKMTKREDGGYTFATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASC
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQ
AQETLKS LGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

TGGCCTCCCCAGCTTGCCAGGCCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
CAGTGTTTTTGCCTTCACCCCAAGTGACCATGAGAGGTTGCCACGCGAGTCTCAATCATGCTCC
TCCTAGTAACGTGTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGGTGCGGATGTGCACCCCGCT
GGGGCGGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCCTTCTTCAGGAAACGCA
AGCACCCACACCTGTCTTGTCTTGCCCAACCTGTGTGCTCCAGGTTCCCGGACGGCAGGTAC
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTTAGCGCGCTTGCTGGTCTCAGGATACCCA
CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGAC
TCTCCCAGTCCCTACACTGACTACCTGATCTCTTGTCTAGTACGCACATATGCACACAG
GCAGACATACCTCCCATCAGATGCTGCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
CTGTGGTGTGAAGAGTGGCCAGCCTGGTTCTCTCCCTGCTCAGGCTGCCAGAGAGTGGTGA
AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCAAGGTGACCTGCTCTCTTTCTGGGCCCTG
CCCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
GCATTGCTCAGAGTCCCAGGTCTTGCCCTGACCCTCAGGCCCTTACGTTGAGGTCTGTGAGG
ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
CCTGTGACCTTCTGCCAGAATTGTATGCGTCTGAGGCCCTCTTACCACACTTTACCAGT
TAACCACTGAAGCCCCCAATTCCACAGCTTTTCCATTAAAAATGCAAATGGTGGTGGTTCAA
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCCTTTCCA
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTTGTCCAGATTGGGG
TGGGAGCAAGGGCAGGGGACGGGCAGGGGCTGAAGGGGCACTGATTCAGACCAGGGAGG
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCACCTGAAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGGCGCCGGGCGTCGGGGCGGTAAAGGCCGCGCAGAAGGGAGGCACCTTGAGAAATGCTCTTCT
 CTCCAGGACCCAAAGTTTCTTACCATTGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCAGAAAGCGG
 CCTGGAGTACCTGGAGGATATAGACCTGAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAGAGGACTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCTGAGAGGAAGCTGCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAGTTCTATGGTCCACAAGCGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACTTCTCCGAGCTGGAACGGAG
 GCTTCTGTGAAACCTGGAAGGAGAAAGGCTTCATCCTTGGGGGAGTTTCTGTGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGTAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT
 GTTTCACCTCGTGTCCCTAAGGAGTGAGAAACCATTTATACTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATATTAAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTGGGAGTTTCAGACACAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAATCACCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGCTGTAGCAGGAGAAATCACTTGAACCTGGGAGGTGGAGTTTCGGTGAGCTGAGATCA
 CACCATTGGATTCTCAGCCTGGGTGACTGAGACTGACTTAACATAA

MSFLQDPSFTTMGWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEADLSSLKSLMDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFKYGPQRKMMFMFGIRLGVVYNFFRAWNGGFSNLEGEFGFILGGVFV
VGSGKQGITLLEHREKEFGDKVNLVSVLEAAKMIKPQTLEASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG
 GGCCAGGTGCCCCGTGCGAGGTGCCCCTGGCCGAGATGCGGTAGGAGGGGCGAGCGCGAGA
 AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG
 CTTCTGGCGCTGGGCCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
 GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
 GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
 CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
 CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
 ACTCCAAGGAGACGGTGCAGGGCTGCCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCC
 CTTTATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
 TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAAGAGAGGATGGG
 GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

270/330

AAATATATCATCTATTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTTGGAGATCCAATTGAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAGAGAAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTAAATTCCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAGAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAAATCAGTAACTGATTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCCTTACAGAATTGACATTTTAA
ATCGCATACAGTTAGAATTAGGAATATGACATTAGAAAGGAAGAATGACAGGGGAGAAAGGAA
AGAAGGGGAAATGTTGCCAAGGAAAAAAA

272/330

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

0909727.11444

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTTATTTCAGAGGTTTGTGTTTCTCTTAGTTCT
 GTGCCCTGCTGCACCACTCAAACTACTTCCTTCATTAAGCTGAATAAATATGGCTTTGAAGATA
 TTGTCTATTGTTATAGATCTACTAGTGTGCCAGAAGATGAAAAAATTAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATTAATTTCTAGAAATTTGAAGGAAAATCTCAGTACAAAAGGCCAAAACAT
 AAAACCATAAACATGCTGATGTTATAGTTGACCAACCTACACTCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTCCAGAGAAATGTGGAGAGAAAAGGCCAATACATCTCACTCACCCCTGACCT
 TCTACTTGGAAAAAACAAAATGAATATGGACCACCAAGCAAACTGTTTGCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTCTTTCATGAGTACAATGAAGATCAGCCTTTCTACCGTGCTAAG
 TCAAAAAAATCGAAGCAACAAGCTGTTCCGAGGTATCTCTGGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGCGAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACGTATG
 GAAAAGATTGCAATTTCTTCTGATAAAGTACAAAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCGTGTTGAAATTTTGAACGAAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAAAAACATAAAGTGCATTTTGAAGTACATGGGAGGTGATTAGCAATTCAGAGATT
 TTTAAACCAACCATACCCATGGTGACACCACTCTCCACCTGTCTTCATTGCTGAAGATC
 AGTCAAGAATTTTGTGTCTTAGTCTTGTATAGCTTGGAAAGCATGGGGGGTAAAGACCGCT
 AAATCGAATGAATCAAGCAGCAAAAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGG
 TGGGATGGGTTCACCTTTGATATCTACTGCCACTATTTGTAATAAGCTAATCCAAATAAAAAGC
 AGTGAAGAAAGAACCACTCATGGCAGGATTACCTACATATCTCTGGGAGGAATCCCAT
 CTGCTCIGGAATTAATATGCTTTTCAAGTGATTGGAGAGCTACATTTCCCACTCGATGGAT
 CCAAGATCTCTCTGTGCTGATGGGGAGGATAACACTGCAAGTCTTTGTATTGATGAAGT
 AAGCAAGCTGGGCCATTGTTTATTTTATGCTTTGGGAAGCTGCTGATGAAGCAGTAAAT
 AGAGATAGCAGAGATAACAGGAGGAAGTCATTTTATGTTTTCAGATGAAGGTCAAGACAAATG
 GCTCTGAAATGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAGTCCCTT
 CAGCTCGAAAGTAAAGGATTAACTCATGAATAGTAATGCCTGGATGAACGACACTGTCAATAAT
 TGATGATACAGTGGGAAGGACACGTTCTTTCTCATCAGTGAACAGCTCTGCCTCCAGTA
 TTTCTCTCTGGGATCCAGTTCGAACAATAATGAAAAATTCGACAGTGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTCAGGAACTGCAAGGTTGGGCACTTGGGACATCAATTTCAAGC
 CAAGCGAACCCAGCAAACTTAACATTTACAGTAACCTCTCGAGCAGCAAAATCTTTCTGTGC
 CTCCAATCAGAGTGAATGCTAAAAATGAATAAGGACGTAACAGTTTCCCGAGCCCAATGATT
 GTTTACGCAAGAAATTTACAGGATATGTACCTGTTCTTGGAGCAATGTGACTGCTTTTAT
 TGAATCAGAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGAGGCGCTGATT
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAAATGGCAGATAT
 AGCTTAAAAAGTTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAAATACGGGCTCCACT
 GAATGAAGCCGCGTACATAACAGGCTGGGTAGTGAAACGGGGAATTTGAAGCAAAACCCGCCAA
 GAGCTGAATTTGATGAGGATACTCAGACCACTTGGAGGATTCTGAGCCGAACAGCATCCGGA
 GTTCGATTTGTGGTATCACAAAGTCCCAAGCCTTCCTTGCCTTGACCAATACCCCAAGTCA
 AATCAGACAGCTTTGATGCCACAGTTCATGAGGATAAGATTATTTCTTACATGGACAGCAGCAG
 GAGATAATTTTGAAGTTGGAAAAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATTTCTT
 GATCTTAAGAGCAGTTTGTATGATGCTCTCAAGTAAATACTACTGATCTGTCAACAAAGGA
 GGCCAACTCCAAGGAAGCTTTGCAATTTAAACCAGAAAAATCTCAGAAAGAAATGCAACCTT
 ACATATTTATTTGCCATTTAAAGATATAGATAAAAGCAATTTGACATCAAAAGTATCCAACTT
 GCACAGTAAGTCTTTGTTATCTCCCTCAAGCAAACTCTGATGACATTGATCCTTACACTCTCT
 TACTCTACTCTACTCTCTGATAAAAGTCATAATCTGGAGTTTAAATTTTCTACCTGGTAT
 TGCTGTGATTGGGTCTGTTGTAATTTGTTAACTTTATTTTAAATACCACTTT**GA**CACTTAA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGGTTTAAAAAACCAAAACATGTAGT
 AAAGATATTTCTGAATCTTAAATATCATCCCATGTGTGATCATAAACTCATAAAAATTAAT
 TTAAGATGTGGGAAGGATACTTTGATTAATAAAACACTCATGGATATGTAAAAACTGT
 CAAGATAAAAATTAATAGTTTTCATTTATTTGTTATTTTGTGAAGAAATAGTGATGAAC
 AAAGATCCTTTTCTACTGATACCTGGTTGTATATTTATTTGATGCAACAGTCTTTCTGAAT
 GATATTTCAAATTTGCATCAAGAAAAATAAAATCATCTGAGTAGTCAAAATCAAGATAAA
 GGAGAGCAAAATAACAACTTTGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 274

MGLFRGFVFLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY
 LFEATEKRFFFKNVSLIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKNFRSTWEVISNSEDfKNTIPMVTPTPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRNLNRMQAACHFLLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFILESQNGHTEVLELLDNGAGADSFKNDDGVYSRYFTAYTENGYSGLKVRHAG
 GANTARLKLRLPLNRAAYIPGWVNVGEIEANPPRPEIDEDTQTTLDEDFSRITASGGFAVVSQV
 PSLPLPDQYPPSQITDLDATVHEDKIILTWTPAGDNFDVGKVQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAGACCATTACGTCCCCG
GGCAGGGGTGACACAGGTTGCTATCTTTTGTATCTCGTGTGTGGCTGCCCTTCTATTTCAGGAAAG
AGCCCAAGGTAAATTTGACCACAGGAGCAATGATGAGCCACCTTCTAACCTTCCCTTCTTGAACC
CCAGTTTATGCGAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTT
GTGGTTGGAGGAGAGAACTTTGTGGGGTGCCTTCTTTAGCAGTGTCTCAGAACTGACTTGCCTGA
GGGTGGACCAAGAAAGAAAGAGGTCCCCCTTGTCTGTGGCTGCACATCAGGAAGGCTGTGATGGG
AATGAAGTGAATACTTGAGATTTCACCTTCAGTCAATTCGCTCTGCAAGATCATCCTTTAAAA
GTAGAGAAAGTGTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTCTAGAGAAGAAATGGATG
CAAGCAGCTCCGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCCAGGGAAGGCCCTTCGGTGGG
GCCCGGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGGTTCGCG
GGGGCTGCTTGCCTGGATTTCCCGGGTGGTGGTTTGTGGTGCCTCTCTGCTGTGCTATCTCTGT
CCTGTACATGTGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGGCACTGCCAGGGCCAAACAGC
CCCACGGGGAAGGAGGCTACACGGCGCTCCTTCAGGAGTGGGAGGAGCAGCACCAGCAACTACGTGA
TGCGGCTTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGGAGGAGGAGCTGACGACCTCAGGAA
GGGCGAGTACCAAGCCAGCATGCTGCTGGCTGGGTCTGGACAGAGCCCCAGGAGAAACCCAGC
GGCAGCTCTCTGCGCTTCTGCACTCTGCAGGTTGGACAAGGCAGAGTGAATGCTGGCTCAAGCTGG
CCACAGACTATCAGCAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG
CCTTATCCCGCCACCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGATGAGTTGGTGGGAAGCCATT
GTATCAGCCTTGGAGACCCCTGAAACAATCTTGCAGAGAAACAGCCCAATCAGCGTCTCTACACGGCTT
CTGATTTTCATGAAGGATCTACCGAACAGAAAGGACAAGGGAATCTGATGAGCTACCTTCTCAA
AGGGGACCAACAACAGCAATTCACACGGCTCATCTTATTTCGACCATCAGCCCACTCATGAAAGT
AAAAATGAAAAGCTCAACTGCGCAACACGCTTATCAATGTTATGCTGCCTCTAGCAAAAAGGGTGG
ACAAAGTCCCGGCGATTCATCGCAATTTCAAGGGAGATGTGCATGTAGCAGGATGGGAGAGTCCATCT
CACTGTGTTGTTTACTTTGGGAAGAAGAAATAAATGAAGTCAAGGAATCTTGAAGAACTTCTCAA
GCTGCCAATCTCAGGAATCTTACCTTCATCCAGCTGAATGGAGAAATTTCTCGGGGAAGGAGCTTG
ATGTTGGAGCCCGCTTCTGGAAGGGAAGCAGCTCCTCTCTCTTTCTGTGTGATGTGCATCTACT
CACATCTGAATCTCTCAATACGTGTGAGGCTGAATACACAGCCAGGGAAGAAGTATTTATCCAGTT
CTTTTCACCTAGTACAACTCTGGCATAAATATACGGCCACCATGATGCATCCCTCCCTTGGAAACAGC
AGCTGCTCTAAAGAAGAAAGCACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTGATATCG
GTCAGACTTCATCAATATAGTGGGTTTGATCTGGACATCAAGGCTGGGGCGGAGAGGATGTGCAC
CTTTATCGCAAGTCTCCACAGCAACCTCATAGTGGTACGGACCGCTGTGCGAGGACTCTCCACCC
TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGCATGACGTCCAA
GGCCATGAACGAGGCGATCCACGGCCAGCTGGGCATGCTGGTGTTCAGCAGCAGATGACAGGCTCAC
CTTCGCAACAGAAACAGAAGCAAGTAGCAAAAAAATCTGAAGTCCCAAGGAAGGATTTGGGAGA
CACTTTTTCTTTCTTTTGAATTTACTGAAAGTGGCTGCAACAGAGAAAGACTTCCATAAAGAGCG
ACAAAGAAATTTGAGTGTAGGGTCAGAGATGAGAAAGCCCTCCGATTTCTCTCTGTGGGCTTTTTAC
AACAGAAATCAAAATCTCCGCTTTGCTCGAAAGATACCCAGTTGCACCCGTGTGAAGTGTGAC
AAGGCAGAAATGCTTTGTGAGATATAAGCTTAATGGTGTGGAGTGTGTGATGGTTTACATATCACT
GAGACCTGTTCTTTGTGTGCTGATGAATATCTGATTTAAGAGCACTTTGTAAATAATTCAT
TAGCATGAAGCGCAAGCATTTCTCTCATATGATGAGCTATCAGGAGGCTCTAGTTTCTAGG
AATGCTAAAATATCAGAAGGCGAGGAGAGATAGGCTTATTATGATATAGTGAGTACATTAAGTA
AAATAAATAGGACCAAGAAAGAAAGCAATTAATATCGTGTCAATTTTCCCAAGATTAACCA
AAAATAATCTGCTTATCTTTTGGTTGCTCTTTAACTGTCTCCGTTTTTCTCTTTTATTTAAAAAT
GCATTTTTTTCCTTTGTGAGTTATAGTCTGCTTATTAACTACCTTTGCAAGCCCTTACAGAGA
GCACAAGTTGGCCTACATTTTATATTTTTAAGAAGATACTTTGAGATGCATTTATGAGAACTTTCA
GTTCAAGCATCAAAATGATGGCCATATCCAAGGACATGCCAAATGCTGATCTGTCAGGCACTGAAT
GTCAGGCATGTAGACATAGGGAAGGAATGGTTGTACTAATACAGACGCTACAGATACCTTCTCTGAA
GAGTATTTTCAAGAGGAGCAACTGAACACTGGAGGAAAGAAATGACACTTTCTGTTTACAGAA
AAGGAACCTCATCAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCCATTTTCTCTCA
GAAGTAGGAGCCGCTTCTTACCTGTTTAAATAAACCAAGATACCGCTGTGACCAACCACTCTCT
TTTCAAAACAGGGTGTCTCTCGGCTTTCGGCTCCATTAAGAGAAATGGAGAAAATATATATAT
ATATATATATATGTGAAGATCAATCCATCTGCCAGATCTGATGGGATGGAAGTTTGTGCTACAT
GTTATCCACCCAGGCGAGGTGGAAGTAACTGAATTTTTTAAATAAGCACTTCTACTCAATCA
CCAAGATGCTTCTGAAATTTGCATTTTATTACCAATTTCAAACATTTTTTAAAAATTAATACAGTA
ACATAGAGTGGTTTCTTCATTTCATGTGAAAATTTATGCCAGCAGCAGATGAGCTAAATATCT
CTTTGAGTCCTTGTCTGTGTTGCTCAGAGTAACTGATGTTTAAAGCTTCAAGAACATCTCAAGC
TGTTGGTGTGTAAAAAATGCATTGATTGATTTGACTGGTATGTTGAATTTTAAATAAACAC
AGGCCATGAATGGAAGTGGTATTGCACAGCTAATAAATATGATTTTGTGATATGAA

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FIGURE 276

MMMVRRGLLAWISRNVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ
 EWEEQHRNYVSSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
 HSQVDKAEVNAGVKLATEYAAPVFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDELVEAIES
 ALETLNNP AENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPI
 MKVKNEKLN MANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
 GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
 LNTQPGKKVFPVLF SQYNPGI IYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
 NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPV RGLFHLWHEKRCMDELTP EQYKMC MQS
 KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTS SKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTGTTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCTTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTCTTTTGTAATAAATTTTGAATGTGCT
 TGAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC
 TCAAAATATTCTAAAATATTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTGTACGATCACTTATATCACTCTGTATATGACTAAGTAACAAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCTAATAGGAC
 AATTCTATTTGTTGACCATTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

278/330

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPs

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FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGT
 ATGGCAAGAGCTCTACTCGTGCCTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTAGAAAGACACAGACTTAAACAATTTTAGATGGAAGCTGAGATGATTCCAAGAACA
 GAACCCTAGTATTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATACCAAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTCAGA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGCTGTTACATTTCTTTTACAGTATTCTTTTAGCAGCATTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTCTTCTCCACATTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAACAGTAAATCTAAATCAAACGTGTTAAATGACATTTTATTTTATGTCTC
 TCCTTAACATAGAGACACATCTTGTCTTACTGAATTTCTTCAATATTCAGGTGATAGATT
 TTTGTCTG

FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILWKLQFDDNGTYTCQ
VKNPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLQHYRKKRWAER
AHKVVEIKSKEERLNQEKKVSVYLEDTD

FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTCATGCTTCCTGTGATTTT
ATCCAACCTACTTACCTTGCCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

FIGURE 282

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

282/330

FIGURE 285

GTCA**ATC**GCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTGACAGTGGGCCAGGCCCTCAACGGTGTGTACAGGACCAGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTACAG
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTGTAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGGAGATGGTGGCACAGCAGCATCGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGGCC**TGA**ATCTGCCTGGATGGAACCTGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCGGGGCCCACTTCTGAGCACAGAGCAGAGACAGAC
CAGGGCGGGGACA**AA**GGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTTC**CA**AAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

286/330

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTL LFHGT LQLGQALNGVYRTTEGR LTK
ARNSLGLYGR TIEL LGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMV AQQHRLRQ
IQR LHTAALPA

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FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAGAATGGACTTGTAAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAAGTCAATGCCTTGAAGGAAATTCAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAATGTGTCCTGTTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCTGTGCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAA**ATAG**GTCTTTCTCCAATGTGTCTCCAAGCAAGATTATCATATACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAAAAAATTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCTT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAATCTTTCTCTCTAGTCTTTCTCACTTGACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGAAGTTTAGCGTATGTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCTCCATGCTGGCAATAATACC
 TTGTGAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTTGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
 CAATTTTCATTTCCACCATTGCATTACAACTCTAACTTAAATGGGTAACCTTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAACTCTATTATGGGCAACCAATCTT
 TGGAGCTGAAAACCTGAATTTAAAGAAATGCTATCTTGGAAAAATGCATACGCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTTAGAAGCAAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACCTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTCTATGCTCA
 ATAATAAAGCCTGAATCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

288/330

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

288/330

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGACGGTTCCCCGCGCGC
 CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
 GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
 GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCCTGGCCAACCCCTCGGCACCCCTCAACCCGCT
 GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
 GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
 GCCCTGACAGTGTTTGGC**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
 CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT
 CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAC
 CCTTGGCCTCCGACGCGCATCACATGAAGGTGGTGCCAAAGTCTCCTGCTCTCCGTCCTCCTG
 GCACAGGTGTGGCTGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTCGGATTGAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGACAGGCCCTGAAGCCCAACAG
 CCCGGGCTCTGCTTCCCTCTTTAAGGACTCAGAGAGACCTCTCCCGCAACCTGGAAC
 GGGCTCTCACAGGGGAGTTTGGCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAATTTCCAAACT
 GTTTGATGAGATTAATCCTGAAACCAATTAATCTTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCCCTGTCTTACCAGAGTGCACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCATGATGTACGGTGACGGCAAGTTTGCTCCACCTTTGACAAGAA
 TTTTCGTTGTCTGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA
 TGGAGAAAATGGGTGACACTCGCCCTGGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACCCAGAACATGGAAGTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAGAACTCTTCTCACCCCTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTGTGCAAAATAC
 TGCTTATTCATGCCCTCTGTCTCAAAGTGGACCGGCCATTTTCATTTATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGACGGGTGGTGAATCCGACTCTCCTATTAATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTTTTTGTTCTTAACTAGTTTLAGGTGTTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACTTATATATATTTTTCTTACATACATACCATGATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA
 CATCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCTCCACTACTCAGAATGGCATGC
 TGCTTTAAGACTTTTAGATTGTTATTTCTGGAATTTTTCATTTAATGTTTTGGACCATGGT
 TGACCATGGTTAACTGAGCTGCAGAAAGCAAAACCATGGATAAGGGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

292/330

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
 GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
 CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
 GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC
 TGTCAGAAAGCCGAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGCAGGGGCCCCCA
 TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCCTGGGCCGTGTCCTGAGTCCC
 GAGCCCGACCATGACAGCCTGTACCACCCCTCCGCTGAGGAGGACCAGGGCGAGGAGAGGCC
 CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
 TCTACCACCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCAAGGCCAGG
 CTGTTGGGACTGGGACCCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
 AAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGPPEEDQDHIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTCCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGCAATTGTATGGCCTGTATTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGCTGGACCCTGGTGGCCAGCGTGATGAGAATGACATG
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCTCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCGAGAAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTCGGGATT
 TGTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
 CCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGAATATGGAACATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTGTG
 GGAGGGAAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHHCIGGGGYFPEASPPQCGDFS GFDWSGYGTHVGYSSSREITEAAVLL
FYR

FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCGGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAATATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTAAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAAATAGTTTAAAAAATATTTCT
 CTTTTTGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCATCTTTTTTTTTTGGCT
 GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAAGTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAAGTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLGLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSEFVGIVLTGLVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGCAGCCCTGTGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCTGGCGCTTCCGTGCTGCTGCTGGC
 GCAGCTGTGAGCGCCGCCAAGAATTTGAGGATGTCAGATGTAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTTGGGATCACCAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGCTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCAGCTAAATTGGGAATTGAATTCAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTAATACCTTGTGATTTCACCAACT
 GTTGCTGGAAGATTCAAACTGGAAGCAAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTG
 TTGTTGTTGTTTTTTGTTGTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
 AACAACTTTTTCAAGTCATTTACTAAACAACTTTGTAAATAGACCTTACCTTCTATTT
 TCGAGTTTCAATTTATATTTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAACGGGAT
 CTAATAATGCCTGGTGGCTTTTACAAAAAGCAGATTTTCTTATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAACATAGTCTTG
 GTGTGTGTTGTTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGA
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACATTTG
 TCAGCATTTCCGGTGTGGTGAGAGGCAGCTGTTGAGCTCCAATATGTGCAGCTTTGAACT
 AGGGCTGGGGTTGTGGGTGCTCTTCTGAAAGGTCTAACCATTATTGGATACTGGCTTTTT
 TCTTCTATGTCTCTTTGGAATGTAACAATAAAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHYKNIS QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERS
SVTIKVTIIIIYLSILGLLLLYMVYLT
L VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLARS
SRANVLNKVEYAQQRWKLQVQEQ
RKS VFD RHV VLS

224999

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGCTCCTGGCTCTGTGCTGCTGCTGCCCCAAGGCCTTCCTGTCCC GCGGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACCTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAAGTGTTTTGCCCAAAATTCAACAATAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTCTTAATCCAGTGAGTGATACAATTCAATGCACCTCCCTGCCA

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FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPIYGFIFLYILYILFKVSRIILI
ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTTGCCCACTGAAACTCATCTGCTGCCAGTGTTC
 TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAGAT
 AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC GCGTACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTTCAGATGGGATGTGTTTTCCAG
 AGCACAGAAGTAAACACGTGACCAAGGTAGAAATGGATATTTTCAGGACGCGCGCAAAGGA
 GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGG
 GCCACTTCAGAAATCGTGTGAACCTGGTGGGGGACATTTCCGCAATGACGGTTCCATCATG
 CTTCAAGGAGTGAGGGAGTGCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGCACCCGGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
 GAGTTCAGTGAATCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCTGTGTGTCTCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC
 CCAGCTGTCTCTGTCTCATGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCTCAAACCCCCCGTT
 GGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGTYYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWG HFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPV LILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEK PCHFERCEGEKHIYSPIIVREVIEEEE PSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATGCA**
GGATGAAGATGGATAACATCACCTTAAATATTTAAACTCGGAAACCAGCTCTCGTCTCCGTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGAGATATTATGGAGATAGCTGCTATGGGTCTTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWVRMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

CCACACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGGATCCCGC
CCCGGGGTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTCGGGAGAA
GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCGAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGCGCGGCGGTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTACGAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAGTTAATGTCTTTTCCCGGCTCAAACTCTTCGGCTCCAAGAGAGGCGCAG
AAGAAGACCAAGGCTTACGTTAAGGTATAGTTACCAAGCTATACGCGGACAGAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCAATTGATGCGACCAAGAATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTGTGAAAATTATTATGTGACATATTTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAGCCTCGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGCCATGT
ACAAGGAGCCATCACTGCAGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGCTCTTGGCGTGTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGGAGGCTCTGTAACAGAGTCTTACCTCCAGGTCTGTTGAAT
CTCTTGTAGCAGTCTCTCACCAAAAGTCAAATTTGACCTGACATTACCAACCAACAGG
CAGTGTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACATAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKDEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGATTTCAGTGAAAAAAGTGGGGGATCCCTT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCTTCTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCACACCCCTGTAGATTAC
 AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGTCCCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGCGAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGCTGTCTGG
 CGCAGCGGCGCGTGTGTCCCCCGCGCACCAAGTCCCTTTGCCAGAAGCAGTCCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCGCGCGGCCGAGCCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACCTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCTCCTCACCCACTTCAACCTGATCCCT
 GTGGGCCCTCCGTGTGGTCAACATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCTGTCTGCGCGGCC
 TGGTACCTCGGCTGGACAAGGAGGGCCAGGTCATGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKSLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGCGGAGCAGCCCCAGCAAGAACCGGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAACACAGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAATAATTATATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRRLR
RQDPQLKGIIVTRLYCRQGYIQLMHPDGDALDGTCKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCITGCAAAAAT
 GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCAITCAAGAATG
 AATAAACCAGAGTTAGACCCCGGGGGTGGTGTCTGACATAAATAAATAATCTTAAGACAGCTGTTCCTCC
 CTCCTCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCAGGAGTTCACAAAGAAAAAGTATGTTTCATT
 TTCTCTATAAAGGAGAAAGTGACCCAAGGAGATATTTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAGATA
 AGAAGCTGGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCACAAAGAGGAGAGAAATAATAATACATCTGC
 AAGAAGATTTCAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTTGTGCCTATGTTGACTAAATTTGACGGATAATGCAGTTGGATTTTCTTCATCAACCTCCTTT
 TTTTTAAATTTTATTCCITTTGGTATCAAGATCATGCGTTTTCTCTGTTCCTTAACCACTGGATTTCCATCT
 GGATGTTGCTGTGATCAGTCTGAATACAACCTGTTGAATTCAGAAAGGACCAACACAGATAAATTATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAAACAGGGCCCTATTGACCCCT
 GCTTGTGGTGTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGCTGGTGGGGCTCAGACCTGCCCTCTGTGT
 GCTCCTGCAGCAACAGTTGAGCAAGGTGATTGTGTTGCGAAAAACCTGCGTGAGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTTCATGAGAACCBAATCCAGATCATCAAGTGAACAGCTTCAAGCATTGAG
 GCACCTTGAATACTCAGATTTGATGAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTTTGACAACTCGTCTTACTACCATCCGAATGGAGCTTTGTATACCTGTCTAAA
 CTGAAGAGGCTCTGGTTGCGAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTT
 GCGCGACTAGACTTAGGGGAATTGAAAAGCTTTCATACATCTCAGAAGGTGCCITTTGAAGGTCTGCCAAT
 TGAGGTATTTGAACCTTGGCATGTGCAACCTTCGGGAATCCCTAACCTCACACCGCTATAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTATCTGCCATCAGGCTGGCTCTTCCAGGGTTTGTATGCACCTTCAAAAACT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCITTGACAACCTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCCTCATGACCTCTTCACTCCCTTGCATCATCTAGACGGATACAT
 TTACATCACAAACCCTTGAACCTGTAACCTGTGACATACTGTGGCTCAGCTGGTGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCGCGGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTTGATTACTCCAAATGGAACAGTCAATGACACA
 TGGGGCGTACAAAGTCGGATAGCTGTGCTCAGTGTGAGTACGTTAAATTTTCAAAATGTAAGTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGAGTAATTCGGTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAG
 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTGCAGTGGGAGACCAATATGTGACCCTCTCTCACAC
 CACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAAT
 GATGAGGTGATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCAGACTCATGGCTGCAGTATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATTCGGCAAAACCATCACGCCCCAACAGGACTGTTGAARTTA
 TTAATGTGGATGATGAGATTACGGGAGACACCCATGGAAGGCCACTGCCCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAGTAAACACAATAAATAACATA
 CAGTTTCAGTGCATGAACCGTTATTGATCCGAATGAACCTTAAAGACAATGACAGAGAGCTCAAACTCAAAACA
 TTTACAGAGTTTACAAAAAACCAACAATCAAAAAAAGACAGTTTATTAATAAATGACACAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGCTTTTCAAAAAAACAAAAAGAAAGAAATTTATTTATTAATAATCTATTG
 TGATCTAAAGCAGACAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRLFDPLLVLALLQLLVVAGLVRAQTCPSPVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTELEFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNRLRYLNLA MCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASLTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLFTNVTVQDTGMYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTFVVDWETNVTTSLTPQ
STRSTEKTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

CGCGCCGGGAGGCCATCTGCCCCAGGGGCACAGGGCGCGGGGCCGGCTCCGCCCCGGCACAT
GGCTTGCAGCCACCTCGCGCGACCCAGGAGCGCGCGCCAGCTCGGCCAGGTCGCTCGGA
GGCGCCGGCGCGCCGGAGGCCAAGCAGCAAGCTGAGCGGGAAGCGCCGGCTCGGGGATC
GGC**ATG**TCCCTCCTCTCTCTCTTGTCTAGTTCTACTATGTGTGAACCTTGGGGACATCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAGGTTCACTTGTCCCTGCCACCATCACTGGGC
TTCAGAAAAAGACACTCTGGATATTGAATGGCTGCTACCCGATAATGAAGGAAACAAAAA
GTGGTGATCACTTACTCTAGCTCGTACTGTCTACAATACTTGACTGAGGAACAGAAGGCCG
AGTGGCCTTTGCTTCCAATTCTCGGACGAGGATGCCTCTTGCAGATTGAACCTTGAAG
CCAGTGTGAGGGCGGTACACCTGTAAGGTTAAGAATTAGGGCGCTACGTGTGGAGCCAT
GTCTATCTTAAAGCTCTTAGTGCAGACCTCAAGCCAAAGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTCTTTCAGTGTGAGTCACTCTCGGCACAGACCCATCTGTGTTAT
ACTGCGACCGAATCCGAGAGAAGGAGGAGATGAAGCTCTGCCTCCCAATCTAGGATT
GACTACAACCCCTGGACAGAGTTCTGTGTCAGAAATCTACCATTCTCTGACTGTAT
CCAGTGCACAGCGAGGCAAGCTGGGAAGGAAAGCTGTGTGGTGGCAGTAGTCTGTACAGT
ATGTACAAGAAGCTCGGACTGGTTGTGACGAGGAGCAGTGACAGGCTAGTGCTGGAGCCCTGCA
ATTTTCTCTTGGTGTGCTGCTACTGACTCCGAAGGAAGACAAAGAAAGTATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCTCTGAGCTCTCGGAGCTCAGCTCTGTGTTCTTCTCCATCTCGCTCCACAGAAAT
AGTGCTCAAGCAGCGACCGAGACCTGTCACTCAGCAGCAACCCAGCCAGGCGTGGCCAC
CCAGGCATACAGCTGTGTGGGCGCAGAGGTGAGAGGTTCTGAACCAAGAAGTCCACCATT
CTAATCTGACCAAGCAGAAACCCAGACCTGATCCCCAGCCAGAGCAGAGCTTCCAA
ACGGTCT**GA**ATTACAATGGACTTGACTCCACGCTTTCCTAGAGTACAGGTTCTTTGGACTC
TTCTCGTCAATTGAGCTCAAGTCAAGCCACAGCAACACAGATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGACGGAAACAGATTTCAGATGACATTTTCTTATACATACCAAACAGCAAA
AGGATGTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCGAGGATCCAAATCTATTGTTGACAGGACCTGTGGTGGAAGGTTGGGGAAGAGTG
AGGTAATATACCTAAACCTTTTAATGTGGGATATTTGTATCAGTGGTTGATTACCAAAAT
TTCAAGAGGAATGGGATGCTGTTGTAAATTTTCTATGCATTTCTGCAAACTTATGGATT
ATTAGTTATTTCAGACAGTCAAGCAAGCCACAGCCTTATTACACCTGTCTACACCTGTAC
TGAGCTAACCACTTCTAAGAAATCCAAAAAGGAAACATGTGCTCTTATTCTGACTTAAC
TTCATTGTCTATAAGGTTTGGATATTAAATTTCAAGGGAGTGAAATAGTGGGAGATGGAGA
AGAGTGAAATGAGTTTCTCCACTCTATCTAATCTCATATTGTGTTATTGAGCCAAAATAC
TATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCATCTCTCATGTGTT
ATGAGGATTGTTGACAACAACTAGAATAATATAATGAGCAATTTGTGATTTCCTTCAAT
CAGATGCTCTATAAGGACTTCTCTGTAGATATTCTTGGAAAGGAGAAATAACAATGTCTATT
TATCAAGCTCTTAGAAAGAAATCTTCTAGAGAAAGGAGTCTAGAATGCTGAAGAGTTA
CCCAACATACCATTATAGTCTCTTCTTCTGAGAAATGTGAACCAAGAAATGCAAGACTGG
GTGGACTAGAAAGGAGGATTAGATCAGTTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGCA
TGGTGCCAGGCACCTGTAGGAATAATCCAGAGGTTGAGGTGCAAGTGAAGCCAGAGATTATGCC
ATTGACCTCCAGCTGGGTGACAGAGCGGAGCTCCGTTCT

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELEGTSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGFEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCCTACCTGCAGCCGCCGCCACGGCACGGCAGCCAA
 CCTGCGCGCTCCTGCTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTCGCCAGAAAGTTTGAGTATCACTACT
 CCTGAAGAGATGATTGA AAAAGCCAAAGGGGAACTGCCTATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CCAGGAGCCCTGACACATCGATGGCTGATATCACCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTAT
 ATCTCGAGACAAAAATTTATGATGACTACTATCCAGATCTGAAGGCCGAGTACATTTTACGAGTAAATGATCTC
 AAAATCTGGTGTGATGCATCAATAAATGTAACCAATTTTACAACCTGTGAGATATTTGCCACATATCAGTGCAGAAATGAA
 AAAAGCTCCTGGTGTGCAAAATAGAAGATTTCATCTGCTACTCTGTAAGCTTCAGGTCCGAGATGTATACG
 TTGATGGATCTGAAGAAATTTGAAGCTGACTTTAAGTAAATGTGAACCAAAAGAGCTTCACTTCCATTACAG
 TATGAGTGGCAAAAATTTGCTGACTCACAGAAAATGCCACTTCATGGTTAGCAAAATGACTTTCATCTGTTAT
 ATCTGTAAAAAATGCCTCTCTTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCCTGTTGCGCTTAACAGTTTGCCTCCTTCAAAATAAGCTGGACTAATTCAGGAGGCCATTATAGGAAT
 TTGCTTGCTCTAGCGCTCATTGGTCTTATCATCTTTTGCTGTGTA AAAAGCCGAGAGAA AAAAATATGAAA
 GGAAGTTCATCAGATATCAGGGAAGATGTGCCACCTCCAAAGAGCCGTACGTCCACTGCCAGAGCTACATCG
 GCAGTAATCATTCATCCTGGGGTCCATGTCTCCTTCCAACATGGAAGGATATTCAGAGCTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAAGTACCTTACAA
 GACTGATGGAATTTACAGTTGTAATAATATGGACTACTGAAGATCTGAAGATTGTATTATTTGACTTTATTTT
 AGGCCCTCTAGTAAAGACTTTAAATGTTTTTAAAAAAGCACAGGACACAGAGATTAGAGCAGCTGTAAAGAACAC
 ATCTACTTTATGCAATTGGCATTAGACATGTAAGTCAGATGTCATGTCAAATTAGTACGAGCCAAATTTCTTTGT
 TAAAAAACCTATGTATAGTGACACTGATAGTTAAAGATGTTTATTATATTTTCAATACTACCCTAACAA
 ATTTTAACTTTTCAATATGCATATCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTCAA
 AGGAAATTTTAAATCTTACGTTCTGTTTAAATGTTTTGCTATTTAGTAAATACATTGAAGGGAAATACCCG
 TTTCTTTCCCTTTTATGCACACACAGAAACACGCGTTGTCATGCCTCAACTATTTTTTATTTGCAACTACA
 TGATTTACACACAATCTCTTAAACACGACATAAAATAGATTTCTTGATATAAAATACTTACATACGCTCCA
 TAAAGTAAATTTCAAAGGTGCTAGAACAATCGTCCACTCTCAGTGTTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAATCTCAAGTCCAATATTA AAAAATTTAGGCACCTTGACTAATCTTAAATAAAATTTCTCAAACATA
 TATCAATATCTAAAGTGCATATATTTTAAAGAAAGATTATCTCAATAACTTCTATAAAAATAAGTTTGATGG
 TTTGGCCCATCTAATCTCAGTACTATTAGTAAGAACTTTAATCTTTAATGTGTAGTAGAGGTTTATTTACCTT
 TTTCTACACATGACACCAACACAACTCAAAAACGAATTTAGTGAGGTGCTAAGCATGTGAGGATTAACTCAGTGAT
 TCCGCTCAGATGCAATTCAGTCCAGGAGGAGTACCCATGTCACTGGAATTTGGGCGATATGGTTTATTTTTCTTCCC
 TGATTTGATTAACCAATGGAACAGAGGAGGATAGTGATTCTGATGGCCATTCCCTCGATACATTTCTGGCTT
 TTTTCTGGCAAGGGTGGCCACTTGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT
 TAAGTTAATTTCAAAGGAAAAATCATCATCTATGTTCCAGATTTCTCATTAAGACAAAGTTACCCACACACT
 GAGATCACATCTAAGTGACACTCCTATTGTGACGCTTAAATACATTA AAAACCTCATGTTAATAGCGGTATAA
 TGTATAACAGGTGACCATGTTTTCTGAATGCCATAAAGAAATGAATAAATCAACACAGTACTTCTTAACAA
 CTCAACCAAAAAAGACCAATATGGAACGAATGGAAGCTTTGAAGGACATGCTGTTTATGTCAGTGGTT
 CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAAACATTGGAGCTGGAGGCCATTATCTCT
 AGCAACTAATGCAGAAACAGAAATCAACTACCGCATGTCTCACTTATAAGTGGAGGTAAATGATAAGACT
 TATGAACACAAAGAGGAAACAAATAGACATTTGGAGTCTATTTTGAGAGGGGAGGTTGGGAGAGGAAAGGAGCA
 GAAAAGATAACTATTGAGTACTGCCCTCACACCTGGGTGATGAATAATATCTACACAAATCCTCTGTGACCA
 TGTTTACCTATGGAAACAACTTTCATGTGATCCCTAAACCTAAATAAAGTTAAAAAAA AAAAAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVDFARSL SITTP EEMIEKAKGETAYLPCKFTLSPEDQG PLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARC YVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGS DQCLLR LNVVPPSNKAGLIAGAIIGTLL
ALALIGLII FCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGMSPSNM
EGYSKTQYNQVPS EDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

[illegible]

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPILLATASQMCMVVLPCLGFTLLWSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCCGAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCGTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCAFTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTCTCTACA
TGCAGAAAACCTCTGCGGCAATGTGAGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACATATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCCAAAAAGTCAAGTGTGGTAT
TTGTAAATAAACTTATCTGTCTGAAAGGGCTCGAGCCATCTCGGGAGCTAAAGGCTGCCCT
CCATCTCAATTTATGTGAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAAGTGATATCTCT
GTAGTACACATTGTACTGAGTGGTTTTCTGAAATAAATTCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVITLST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
 GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTGGATCACACTATTTGAC
 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
 TCAGTATCACTTCTCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCTGCCAGGCATGAACC
 CACCCCCGTACTCCAGTTCCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACC
 CCCATACCAACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCGAACGT
 GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCTCCTGTTACAGGAGCTCCCGAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGTGGTCAGGGGCGGTCGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCG
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLTYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENC RFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRRNEIPLIHFNTPIPRRHTRS AEDDSE
RDPLNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGC**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGTCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGCGCCCATTTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTG
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAACTAAGGGCCTGTCTCTCAGAGAGCAGTGCCCTTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGCTACGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
 GTCACGGGCCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGAGTGGGCAAAACAAGTTCT
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAAGTTACCC
 CTTTCAGAGACCCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACGAGCAGGACCCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCGGAC
 GAGGCCGACCACAGACG**TGAG**TGCAGGTGAAAATGGAGTTTCTCTCTCTGCGGTGAGTG
 TGGCTTCCCCGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCACGCGCTCACTTCCAGGTCTCTTACTGCGTGTCAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCACTAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCTGCA
 TTAATAATCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLPAGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISFARETRSFRTKSPNFMVLIATSVETSAAGSPEGAGM
 TTVQTITGSDPEEAI FDTLCTDDSSSEAKTLTMDILTLAHTSTEAKGLSSESSASSDGP
 HVPITPSRASESSASSDGPHPVITPSRASESSASSDGPHEVITPSWSPGSDVTLLEALVT
 VTNIEVINC SITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVT
 ASAETLSTAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSRNPLEETS
 SALSVETPSYVKVSGAAPVSI EAGSAVGKTTSFAGSSASSYPSEALKNFTPSETPTMDI
 ATKGPFFTSRDPLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCCGCGCGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAAGCTTCTTAAAGCAAACATAAGACCAGAGGGAGGATAT
 CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAA**AATG**TTCTTCGGGGGAGAGGGAG
 CTTGACTTACACTTTGGTAATAATTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCAATTAATTTCTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAAATTTTACAAAGCAGTCACTCCCC
 TAGCCCATCATCACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTTATAAGGAAAAAGGCCATTCTCAGAGTTTCAAAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATAACACCTCGGCTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCAGCACCTCATTTTCTACAGTTTTTACAGGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACTTTTACAGGCACTACGGACTCGAAAGGCAGCTTAGA
 AACCATAACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCTTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAATGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCTGTTCTGGGTATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATC**TAAG**GATGGAACCTCGGTCTCTCTTAATTCATT
 TAGTAACCAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAAATGCCCTTCTGCTTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGAACCTCCGCTC
 CTGGGTCAAGCGATTCTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTAGTAGAGACGGGGTTTCCACCATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCTCGGCTCCCAAAGTCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCTTCTGTTTTATGTTTGGTTTTTGGAGAGGATGAAGTG
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAGTATAATTGCCATATAAATTTCAAATTCACCTGGCTTTTATGCAAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTCTTTTATATGGAATCTTTTAAACCTATT
 CCAGATGTAGTTCCTTCCAATTAATATTTGAATAAATCTTTTGTTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIIICFLTLRLSASQNCLESDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGCGCCCCAGAAATGCGGCTTCTGGTCTGTCTATGGGGTGGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTGCTGCTCTGGCACCATCTATGCAGAAAGAGGGCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTGCTTTCCAGGACCTGCTGTCTCCCTCCCTCTTCCAC
 CTTCCAGCCTCTGGCTACAACACGCTGCAGCCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGCAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCCCCCCCCTATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCGTGTGCTGAGCCTTCTGTACGC
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGCAAGCAAGTTCCTGGCTCTCAGCCTTGAGCTCGGAGGAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGGACGTGATCTCGATGCTCCTCCCTCCACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGTGGCTGGATCAGCACCGGATCCCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCCTCTGCACTGTGCA
 GCCTGACCTAGAACGCTTTGTGACCCCTGGAGCCAGAGCGGTGGCCCTGTCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGG
 CTCATGCCAGTGTGCGACCTGCTTCTCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCACCGTCTCCTGCATCAGCTGGTGATGAAGAGGACATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACACCTGCATCCAGCCCTCAGGAAGCCT
 GTGAAAAACGTGATTCTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCAACAATGCCAGTGACTGTGCACTTGAGTTTGAGGGCCAGTGGGCTGTG
 ATGAACGCTCACACCCCTTACGCTTAGAGTGTGCACTTGGGCTGTGACGTCTCCACCTTGCCC
 CAATAGATCTGCTCTGCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCCTGCTAAG
 TCCAGGCCTTGGTCAGGTGAGGTGCACATTTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
 TTGCTTTNCCATTGGCTCCTGNNCCATGCCTTCTGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTGTCTGAAAGGGTTACTTGCTATGGGTCTGTGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCAGTAGGTGTCTAACACAGAGAGAGTAGGAGAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGGCCCTGAGAAAGGGTGGGGGTGGTGGTAAAGTA
 GCACAACCTACTATTTTTTTCTTTTCCATTATTATGTTTTTAAAGACAGAAATCTCGTGCT
 GTGCTTTNCCATTGGCTCCTGAGTGCAGTCCCAATTTGCCGGATTACAGGCATAGCCCACTGTG
 TCTGGCCCTATTTCTTTTAAAGTGAATTAAGAGTTGTTCAGTATGCAAAATCTGGAAG
 ATGAGAGAGAAAAAGAAAGGAAGAAAAAATGTCAACCATAGTCTCACCAGAGACTATCAT
 TATTTGCTTTTGTGTACTTCTTCCACTCTTTTCTTCTTACATAAATTTGCCGGTGTCTTT
 TTTACAGAGCAATTTATCTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTC
 ATCACTTTATTTCCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAATGTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPPEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCVEKRGPDDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEKAPSQAPEGD
VISMPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128